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Database :
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Listing first 45 summaries
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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24	24	24	24	21	22	13	21	24	BB	
AAD22071	AAD22072	AAD22070	ABI99254	AAC61681	AAD17170	AAQ25722	AAC61678	AAD33667	ID	
Dermacentor variab	Dermacentor variab	Dermacentor variab	Mouse ischaemic co	Nucleotide sequenc	Human ion channel-	GABA-A receptor be	cDNA sequence enco	Human TRICH-22 cDN	Description	

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AAQ33130	AAQ69143	AAQ33131	AAV83111	AAV64372	AAV55008	AAV83112	AAH78309	AAX24373	AA168566	ABL12887	AAI68567	ABL13035	AAH78310	AAD04275	AAD04274	AAD21372	AAX24372	ABI99308	AAD21373	AAD26938	AAT43596	AAD04277	AAD04276	AAD26937	AAQ69141	AAQ33129	AAC61680 .	AAD26939	AAD21397	AAD21396	AAD21395	AAD22082	13	ABK27334	AAT28989
GABA-A receptor al	Human GABA recepto	GABA-A receptor be			 GABA gated chlorid 	an GABA	Nucleotide sequenc	Cat flea glutamate	D. melanogaster li	Drosophila melanog	D. melanogaster li	Drosophila melanog	Nucleotide sequenc	form of S.		Dermacentor variab	\vdash	Mouse ischaemic co	Dermacentor variab	Heliothis sp. HEGM	nate-gate	form of S	form of S	Heliothis sp. HEG3	Human GABA recepto	GABA-A receptor al	Nucleotide sequenc		eus		sanguineus		Juineus	t gamma-	Human GABA-A recep

ALIGNMENTS

RESULT 1 AAD33667 Human TRICH-22 cDNA 01-JUL-2002 (first entry) AAD33667 standard; cDNA; 1874 85

Human; transporter and ion channel; TRICH-22; transport disorder; angina; amyotrophic lateral sclerosis; cystic fibrosis; neuromuscular disorder; cardiac disorder; polymyositis; diabetes; neurological disorder; cancer; depression; schizophrenia; anaemia; Wilson's disease; Cushing's disease; cell proliferated disorder; infertility; arteriosclerosis; gene therapy; Alzheimer's disease; Parkinson's disease; Huntington's disease; allery; myasthenia gravis; multiple sclerosis; metabolic disorder; hypertension; acquired immune deficiency syndrome; immunological disorder; scleroderma; endocrine disorder; autoimmune thyroiditis; rheumatoid arthritis; golitre; cardiac myopathy; annesia; toxic myopathy; Addison's disease; infection; epilepsy; mental disorder; myocarditis; Crohn's disease; Grave's disease; muscle disorder; stroke; dementia; anxiety; AIDS; asthma; cirrhosis;

sapiens.

sig_peptide Location/Qualifiers 286..1539 /product= "Human TRICH-22 protein" 286..369 /*tag= /*tag=

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Ct transport, muscle, neurological, immunological and cell proliferative consists, ataxia telangiectasia, cystic fibrosis, becker's muscular consists, ataxia telangiectasia, cystic fibrosis, becker's muscular consists, ataxia telangiectasia, cystic fibrosis, becker's muscular constitution of the constitut
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10-AUG-2000;
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25-AUG-2000;
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Reddy R,
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08-SEP-2000;
                                            Grave's disease, glomerulonephritis, rheumatoid arthritis, scleroderma, systemic lupus erythematosus, systemic sclerosis, ulcerative colitis, haemodialysis, uveitis; viral, bacterial, fungal, parasitic, protozoal, helminthic infections and trauma; and muscle disorders include cardiac myopathy, myocarditis, polymyositis, arrhythmias and hypertension. The TRICH polynucleotides are used in gene therapy. The present sequence is human TRICH-22 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to human transporter and ion channel polypeptide designated TRICH and nucleic acid molecules encoding such polypeptide TRICH sequences are useful for diagnosis, treatment and prevention of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 96; Page 220-221; 230pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human transporters and ion channels polypeptides and polynucleotides for diagnosing, preventing or treating transport, neurological, muscle, immunological and cell proliferative disorders
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Sequence 1874 BP; 436 A; 510 C; 467 G; 461 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thornton M, Ramkumar J, Tang YT, Azimzai Y, Baughn M, Yao MG, Lal P, Walia NK, Gandhi AR, Hafalia AJA; DB), Patterson C, Elliott VS, Tribouley CM, Lu DAM, X R, Hernandez R, Borowsky ML, Lo TP, Lu Y, Policky JL; BD, Sanjanwala MS, Raumann BE, Burford N, Ison CH, L
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2000US-224456P.
2000US-226410P.
2000US-228140P.
2000US-230067P.
2000US-231434P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    relates to human transporter and ion channel polypeptides
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Query Match

92.8%; Score 1521.2; DB 24; Length 1874;

1080	21 CTCTTTGTGTTTCGCTGCCTTGCTGGAGTATGCTGCCATAAATTTTGTTTCTCGTCAGCAT	Оу 10	
1263	CCTCTTTGCCTAAGGTGTCCTACGTGAAGGCAATCGACATCTGGATGGCTGTGTGTC	Db 120	
1020	61 GCCTCTTTGCCTAAGGTGTCCTACGTGAAGGCAATCGACATCTGGATGGCTGTGTCTG	0у 96	
1203	GTGTGGGCCTGGGCATCACCACCGTGCTCACCATGACCACCCAGAGCTCTGGCTCCCG	Db 11'	
960	01 CGTGTGGGCCTGGGCATCACCACCGTGCTCACCATGACCACCCAGAGCTCTGGCTCCCGG	Qу 9(
1143	CTACTCATCGTCATCCTGTCCTGGGTCTCCTTCTGGATCAACATGGATGCTGCTCCTGCT	Db 108	
900	1 CTACTCATCGTCATCCTGTCCTGGGTCTCCTTCTGGATCAACATGGATGCTGCCC	Qу 84	
1083		10	
840	1 GTAAAGTTTCACCTGGAACGGCAGATGGGCTACTATCTGATTCAGATGTACATCCCCAG	Оу 78	
1023		9	
780 .	1 GAGAAGGATCTAGGCTGTTGTACCAAGCACTACAACACAGGGAAATTCACCTGCATCG	Оу 72	
963	GATGCTCCTGCTGTCCAAGTGGCTGAGGGGCTGACTCTGCCCCAGTTTATCTTGCGGGA	Db 90	
720	1 GATGCTCCTGCTGTCCAAGTGGCTGAGGGGGCTGACTCTGCCCCAGTTTATCTTG	Оу 66	
903	3TTGGCTACACCATGAAAGACCTCGTGTTTGAGTGGCTGG	Db 86	
660	1 CCATCTCTGTCACTTTCAGTTGGCTACACCATGA	Qy 60	
862	6 ATGGACATCCAGACGTGCACGATGCAGCTTGAGAGC	Db 82	
600	1 ATGGACATCCAGACGTGCACGATGCAGCTTGAGAGCTCAT	Qy 54	
. 825	6 CTGTACAGCATCAGGCTGACCCTCATTTTGTCCTGCCTGATGGACCTCAAGAACTTCCC	Db . 76	
540	1 CTGTACAGCATCAGGCTGACCCTCATTTTGTCCTGCCTGATGG	Qу 48	
765	6 AACTTCCATGAGGTGACCACGGACAACAAGTTACTGCGCATCTTCAAGAATGGGAATGT	Db 70	
480	1 AACTTCCATGAGGTGACCACGGACAACAAGTTACTGCGCATCTTC	0у 42	
705	GCTAATGAGAAAGGGGC	Db 64	
420	1 CCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCTTTGCTAATGAGAAAGGGGCC	0у 36	
645	6 CAGTGGAATGACCCACGCCTGTCCTACCGAGAATATCCTGATGACTCTCTGGACCTCGAT	Db 58	
360	AGTGGAATGACCCACGCCTGTCCTACCGAGAATATCCTGATGACTCTCTGGACCTCGAT	Оу . 30	
585	CTTCTTGCGGCAA	Db 52	
300	GTTTCAGCTCCGTCACCAAGACCACAATGGACTACCGGGTGAATGTCTTCTTGCGGCAA	Qy 24	
525	CGGCCCAATTTTAAAGGCCCACCGTGAACGTGACCTGCAACATCTTCATCAAC	Db 46	
240	GGATTCGGCCCÀATTTTAAAGGCCCACCCGTGAACGTGACCTGCAACATCTTCATCAAC	Qy 18:	
465	CCTAGACAAACTTATGGGGCGAACATCTGGATATGATGCC	Db 40	
180	CCATGTCCCCCTCTGATTTCCTAGACAAACTTATGGGGGCGAACATCTGGATATGATGCC	Qy 12:	
405	GGAACCAAGGGGTCCCAG	Db 34	
120	TCCTCCTCAGGGTGGCCTTGGCAAAAGAGGAAGTCAAATCTGGAACCAAGGGGTCCCAG	Qy 6:	
345	1 ATGACAACTCTTGTTCCTGCAACCCTCTCCTTCCTTCTTCTCTGGACCCTGCCAGGGCAG	Qy :	
	Similarity 97.2%; Pred. No. 0; 6; Conservative 0; Mismatches 3; Indels 43; Gaps	Best Local Matches 158	

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 Rappold-Hoerbrand
                 (RAPP/)
                                 26-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein and polynucleotides are useful for diagnosing and treating disorders related to ataxia. Ataxia gene sequences are useful in gene therapy, and as diagnostic tools or reagents for identifying a characterizing genetic defect involved in the disorders and disease related to ataxia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acid sequence encoding human ataxia protein for compounds useful for treating disorders relating to mutations
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DB; AAB19336.
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                       CTGTACAGCATCAGGCTGACCCTCATTTTGTCCTGCCTGATGGACCTCAAGAACTTCCCC
                                                                                                                                                                                    CCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCTTTGCTAATGAGAAGGGGCC
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                                                                                                                                                                                                                                                                                                                                                                                  ATGACAACTCTTGTTCCTGCAACCCTCTCCTTCCTTCTTCTTCTGGACCCTGCCAGGGCAG
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GAGAAGGATCTAGGCTGTTGTACCAAGCACTACAACACAGGGAAATTCACCTGCATCGAG
                                                                                                                                                                                                                            CAGTGGAATGACCCACGCCTGTCCTACCGAGAATATCCTGATGACTCTCTGGACCTCGAT
                                                                                                                                                                                                                                                             AGTTTCAGCTCCGTCACCAAGACCACAATGGACTACCGGGTGAATGTCTTCTTGCGGCAA
                                                                                                                                                                                                                                                                                   CCATCTCTGTCACTTTCAGTTGGCTACACCATGAAAGACCTCGTGTTTGAGTGGCTGGAA
                                                                                      AACTTCCATGAGGTGACCACGGACAACAAGTTACTGCGCATCTTCAAGAATGGGAATGTG
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Pred. No. 0;
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Mismatches
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acid; OmpF;

glycine;

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RESULT 3
AAQ25722
ID AAQ2
XX
AC AAQ2
XX
DT 08-I
XX
DE GABJ
           GABA-A receptor beta-subunit
                                08-DEC-1992
                                                                             AAQ25722 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAGGTCCAATGGAAGGTTCTGGCATTTATAGTCCCCAACCTCCAGCCCCTCTTCTAAGG
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| |||||||||| ||||||
| CCTARARARARARARARARA 1598
                                                                                                                                                                         AGTGCTATGGTCAGAAGATATCCACCAGGCTCTGTGAATAGGGTGGGAGCTATAGAGTCC 1439
                                                                                                                                                                                                                                                                                                         AGTGCTACGGTCAGAAGATATCCACCAGGCTCTGTGAATAGGGTGGGAGCTATAGAGTCC
                                (first entry)
                                                                             DNA;
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Best Local Similarity
Matches 511; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence given is the gamma-aminobutyric acid (GABA) A receptor beta-subunit. This sequence is used in an expression plasmid operably linked to the tac promoter, a ribosome binding sequence, the E. coli outer membrane protein OmpF signal peptide coding sequence and a sequence coding for the N-terminal extracellular site of either the gamma-aminobutyric acid (GABA) A receptor alpha-subunit or the glycine receptor alpha-subunit. This expression plasmid can be used to transform E. coli to produce an N-terminal extracellular site protein of ion channel direct binding type receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prepn. of N-terminal extracellular site protein - l E.coli transformed by a plasmid comprising the tac binding site, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                           CCCAGCCCATGTCCCCCCTCTGATTTCCTAGACAAACTTATGGGGCGAACATCTGGATATG
                                                                                                                                                                                                                                                                                                                                                                                                                                           657 BP; 171
                                                                                                                                                                             TCGATCCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCTTTGCTAATGAGAAAG
                                                                                                                                                                                                                        GGCAACAGTGGAATGACCCACGCCTGTCCTACCGAGAATATCCTGATGACTCTCTGGACC
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               CTCTGCCATCTCTGTCACTTTCAGTTGGCTACACCCATGAAAGACCTCGTGTTTTGAGTGGC
                                                                                          ATGTGCTGTACAGCATCAGGCTGACCCTCATTTTGTCCTGCTGATGGACCTCAAGAACT
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                           22.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           A; 185 C; 156 G; 145 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORP
                                                                                                                                                                                                                                                                                                                                                                                                 Score 366.2; DB 1
pred. No. 1.6e-94;
0; Mismatches 133
       TTGGTTATACCATGAACGACCTCATCTTTGAGTG--
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DB 13; 133;

Indels Length

45;

Gaps

2

415

313

535 373

595 433

509 655 475 355 193

253

133

73

0 other;

by culturing promoter, ribosome

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RESULT 4
AAD17170;
ID AAD17170;
XX AD17170;
XX Human ion channel-93 (lon9)
XX Human; lon channel-93 (lon9)
XX Human; lon channel-93; ions
XX Antiviral; thyroid disorder;
XX Human; lon channel-93; ions
XX Human; lon channel polynucleo
PT CDS

PT CDS

PT CDS

FT CDS

FT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; ion channel-93; ion93; antiinflammatory; immunosuppressive; analgesic; nootropic; neuroprotective; antidepressant; cardiant; cytostatic; antiviral; human immunodeficiency virus; HIV; anorectic; antiviral; thyroid disorder; thyrotoxicosis; myxoedema; renal failure; Crohn's disease; rheumatoid arthritis; autoimmune disorder; pain; stroke; psychotic disorder; neurological disorder; anxiety; dyskinesia; Huntington's disease; degenerative disorder; parkinson's disease; schizophrenia; Alzheimer's disease; cardiovascular disease; cancer; metabolic disorder; anorexia; obesity; mental disorder; ss.
                                                   New ion channel polynucleotides and polypeptides, useful for identification of ion channel modulators and treatment of me disorders, infections, cancer and autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ion channel-93 (ion93) cDNA.
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                     Page 100; 188pp; English
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                                                                                                                                                                                                                                                                 ; 2000US-0188400.
; 2000US-0188517.
; 2000US-0188518.
; 2000US-0188519.
; 2000US-0216815.
; 2000US-0216481.
                                                                                                                                                                                                                                                                                                                                                                                         2001WO-US07503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "Human ion93 protein"
/transl_except= (pos:138..146, aa:Asp-Ala)
/note= "This translational exception comprises
in-frame stop codon insertion; CDS does not inc
start and stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers complement (30..314)
                                                                                                                                                                                               Karnovsky AM,
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                                                    treatment of mental diseases -
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Matches 313; Conserv
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                                                                                                                                                                                                                                                                                                                Human; ataxia; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                     19-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                          AAC61681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC61681 standard;
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29922..
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33752.
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33026.
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33156.
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29850..29921
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The patent discloses novel human ion channel polypeptides and their corresponding polynucleotides. The ion channel sequences and their modulators are used for the treatment of viral infections (e.g., human immunodeficiency virus (HIV)); thyroid disorders (e.g., thyrotoxicosis, myxoedema), renal failure, inflammatory conditions (e.g., Crohn's disease), rheumatoid arthritis, autoimmune disorders, pain, stroke, psychotic and neurological disorders (e.g. anxiety, depression and schizophrenia), dyskinesias (e.g. Huntington's disease), degenerative disorders (e.g., Parkinson's disease, Alzheimer's disease), cardiovascular diseases, cancer, metabolic disorders (e.g. anorexia, obesity) and mental disorders. The present sequence is a cDNA encoding human ion channel-93 (ion93) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 554 BP; 158 A; 124 C; 135 G; 137 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTTCTACTGGGTTGTCTATAAAGTGCTATGGTCAGAAGATATCCACCAGGC-TCTGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AACCTCCAGCCCCTCTTCTAAGGGAAGGAGAAACCACGCGGAAACTCTACGTGGACTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AACGCTTGGAGGAAGATATCATCCAAGAAAGTCGTTTCTATTTCCGTGGCTATGGCTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCAAGAGAATTGACACCATCTCCCGGGCTGTCTTCCCTTTCACTTTTCAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCACTGCCTGCAGGCAAGAGATGGAGGTTCCAATGGAAGGTTCTGGCATTTATAGTCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCAAGAGAATTGACACCATCTCCCGGGCTGTCTTCCCTTTCACTTTCCTCATCTTCAATA
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                                                                                                                                                                                                                                                                                                                                                                                                                         TCTTCTACTGGGTTGTCTATAAAGTGCTACGGTCAGAAGATATCCACCAGGCTTCTGTGA
of the human ataxia gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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No. 2.
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RESULT 6
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents the human ataxia gene. The ataxia protein and polymucleotides are useful for diagnosing and treating disorders related to ataxia. Ataxia gene sequences are useful in gene therapy, and as diagnostic tools or reagents for identifying and characterizing genetic defect involved in the disorders and diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exon
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        Mouse
                              07-MAR-2002
                                                   ABI99254
                                                                      ABI99254 standard;
                                                                                                                                                                                                                                                                                                                                             Sequence 39796 BP; 10630 A;
                                                                                                                                                                                                                                                                                                                                                                   related to ataxia
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          compounds useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (RAPP/) RAPPOLD-HOERBRAND
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                                                                                                                                                                                                                                                                     263 CCACAATGGACTACCGGGTGAATGTCTTCTTGCGGCAACAGTGGAATGACCCACGCCTGT
                                                                                                                                                                                                                                                                                                    232;
        ischaemic
                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Page 22-44; 47pp; English
                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                          CCTACCGAGAATATCCTGATGACTCTCTGGACCTCGATCCCCTCCATGCTGGACTCTATCT
                                                                                                                                     ACAACAAGTTACTGCGCATCTTCAAGAATGGGAATGTGCTGTACAGCATCAGGCTGACC 501
                                                                                                                                                                                GGAAGCCAGACCTCCTTCGCTAATGAGAAAGGGGCCAACTTCCATGAGGTGACCACGG
                                                                                                                                                                                                              CCTACCGAGAATATCCTGATGACTCTCTGGACCTCGATCCCTCCATGCTGGACTCTATCT
                                                                                                                                                                                                                                                         CCTCCCAGGACTACCGGGTGAATGTCTTCTTGCGGCAACAGTGGAATGACCCACGCCTGT
                                                                                                                           ACAACAAGTTACTGCGCATCTTCAAGAATGGGAATGTGCTGTACAGCATCAGGTGCACC 3398;
                                                                                                                                                                     GGAAGCCAGACCTCTTCTTTGCTAATGAGAAAGGGGCCAACTTCCATGAGGTGACCACGG
                                                                                                                                                                                                                                                                                                     Conservative
                             (first entry)
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34115..
        condition
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38782..38996
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35902..3§781
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35760. 35901
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                                                                      cDNA;
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       related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding human ataxia protein for ng disorders relating to mutations
                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                   Score 227.8; DB 2
Pred. No. 7.7e-54;
0; Mismatches 7
                                                                       ВP
                                                                                                                                                                                                                                                                                                                                            C;
        cDNA sequence
                                                                                                                                                                                                                                                                                                                                             9355
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        SEQ ID
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                                                                                                                                                                                                                                                                                                                       Length
        NO:85
                                                                                                                                                                                                                                                                                                                                            other;
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                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        screening in ataxia
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ATGCACTGACAGTTGACCCCACCATGTATAAGTGCTTGTGGAAACCTGACTTATTCTTTG

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ACCTCAAGAACTTCCCCATGGACATCCAGACGTGCACGATGCAGCTTGAGAGCTCATCCA

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343 458 403 403 518 518 578

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                                                                                                                                                                                                      genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB199912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition indicator when screening for ischaemic condition related sequence, which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Examining the ischemic condition (e.g. expression levels of particular genes by determining the expression profile genes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genes
                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                     conditions,
                                                                                                                                                                                                                                                                                                                                                                                                                  The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 265-268; 2690pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ishikawa K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-MAY-2000; 2000JP-0145977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-MAY-2001;
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                                                                                                                               Local
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                230
                                                                                                              503;
                                                                                                                             Similarity
TCTTCATCAACAGTTTCAGCTCCGTCACCAAGACCACAATGGACTACCGGGTGAATGTCT
                                              GTTATGATCCCAGGATCAGACCAAACTTCAAAGGCATTCCTGTTGATGTAGTAGTCAACA
                                                               GATATGATGCCAGGATTCGGCCCAATTTTAAAGGCCCACCCGTGAACGTGACCTGCAACA
                                                                                                                                                                           2404 BP; 705 A; 493 C; 502 G; 704 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                  invention describes a method for examining comprising measuring the expression levels
                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Asai S,
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                                                                                                                            13.5%;
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                                                                                                         0;
                                                                                                           Pred. No. 1.5e
0; Mismatches
                                                                                                                             Score 221; DB 24;
Pred. No. 1.5e-52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . occlusive ischemia) by measuring defined in the specification or of a gene group comprising these
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of particular
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RESULT 7
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GABA-gated chloride channel; recombinant expression; domestic animal;
                                                                                                                                                                                                                                                                                                                                                                                    Dermacentor variabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dermacentor variabilis clone 8 GABA-gated chloride channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD22070 standard;
     New polypeptide useful humans, dogs, cattle, h
                                                                                                                                                                    31-MAR-2000; 2000US-193791P
                                                                                                                                                                                                     28-MAR-2001; 2001WO-US09955
                                                                                                                                                                                                                                                                     WO200174884-A1
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                                                                                                                                    (MERI ) MERCK & CO
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                                                    2002-010778/01.
DB; AAE13312.
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ypeptide useful for preventing or treating dogs, cattle, horses, deer, or other wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGATGCTAGTGCTGCCAGAGTACCTCTGGGCATCTTCTCCGTGCTCAGTTTGGCCTCAG
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                                       ATTCAGATGTACATCCCCAGCCTACTCATCGTCATCCTGTCCTGGGTCTCCTTCTGGATC
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GABA-gated chloride channel; recombinant expression; d
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                                                                                    Sequence 1614 BP; 362 A; 475 C;
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/product= "GABA-gated chloride channel protein"
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55.1%;
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                             CTCGTGTTTGAGTGGCTGGAAGATGCTCCTGCTGTCCAAGTGGCTGAGGGGCTGACTCTG
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ATCTGGATGGCTGTGTGTCTCTTTGTGTTCGCTGCCTTGCTGGAGTATGCTGCCATA 1059
                                                                            ACCCAGAGCTCTGGCTCCCGGGCCTCTTTGCCTAAGGTGTCCTACGTGAAGGCAATCGAC
                                                                                                                     CACCGTGACGCTAGTCCAGCTCGCGTCGCGCTCGCGTCACCACCGTGCTCACGATGACC
                                                                                                                                      AACATGGATGCTGCCCCTGCCCGTGTGGGCCTGGGCATCACCACCGTGCTCACCATGACC
                                                                                                                                                                                 ATCCAGATCTACATCCCGGCCGGATTGATCGTGGTTATTTCCTGGGTCTCCTTTTGGCTC
                                                                                                                                                                                                 ATTCAGATGTACATCCCCAGCCTACTCATCGTCATCCTGTCCTGGGTCTCCTTCTGGATC
                                                                                                                                                                                                                                          GGAAACTACTCCCGCCTGGTATGTGAAATACGGTTCGCCCGCTCCATGGGCTACTACCTG
                                                                                                                                                                                                                                                                        GGGAAATTCACCTGCATCGAGGTAAAGTTTCACCTGGAACGGCAGATGGGCTACTATCTG
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                                                            ACACTCATGTCCAGTACCAACGCAGCGCTGCCCAAAATATCCTACGTCAAGAGTATCGAC
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Best Local
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                                                                                                                                                                                                                                                                                                                                                         The invention relates to gamma-aminobutyric acid (GABA)-gated chloride channels and their corresponding nucleic acid molecules. GABA-gated chloride channel proteins and DMA's are useful for preventing and treating tick infestation, particularly in humans, dogs, cattle, horses, deer, or other wild or domesticated animals. The nucleic acids are useful as hybridisation probes or Polymerase Chain Reaction primers for identifying the presence of Dermacentor variabilis GABA-gated chloride channel nucleic acid or DNA's encoding for a GABA receptor. The nucleic acids are also useful for the recombinant expression of D. variabilis GABA-gated chloride channel proteins. GABA-gated chloride channel proteins GABA-gated chloride channel proteins. The present sequence is Dermacentor variabilis clone 9 GABA-gated chloride channel proteins. The present sequence is Dermacentor variabilis clone 9 GABA-gated chloride channel proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polypeptide useful for preventing or treating tick infestation, humans, dogs, cattle, horses, deer, or other wild or domesticated animals, comprises the Dermacentor variabilis gamma-aminobutyric aci (GABA)-gated chloride channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gamma-aminobutyric acid; GABA; tick infestation; mite; antiparasitic;
GABA-gated chloride channel; recombinant expression; domestic animal; ds
                                                                                                                                                                                                                                                                                                                         Sequence 1614 BP; 371 A; 474 C; 421 G; 348 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; Fig 3; 59pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zheng Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MERI ) MERCK & CO INC
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                                                                       CTCGAGAGCATGACTGTGGGCGCTGAAGTGGCCGAGAGGATCTGGGTACCCGACACCTTC
                                                                                                                                                                       GTCACTATGCAGATTATCAGCATAAGTACAGTCTCTGAAGTACAAATGGACTTTACTTCT
                                                                                                                                                                                     TGCAACATCTTCATCAACAGTTTCAGCTCCGTCACCAAGACCACAATGGACTACCGGGTG
                                                                                                                                                                                                                                             ACATCTGGATATGATGCCAGGATTCGGCCCAATTTTAAAGGCCCCACCCGTGAACGTGACC
                                                                                                                                                                                                                                                                                                                                                   channel DNA.
                                                                                                                       GACTTCTATTTCCGGCAATCGTGGCGGGACGAGCGACTCTCGTTCCAGAAAAGCCCCAGAC
                                                                                                                                              AATGTCTTCTTGCGGCAACAGTGGAATGACCCACGCCTGTCCTACCGAGAATATCCTGA-
TTTGCTAATGAGAAAGGGGCCAACTTCCATGAGGTGACCACGGACAACAAGTTACTGCGC
                                                                                                                                                                                                                       ACACGTGGGTACGACAGGAGGGTGAGGCCAAATTATGGCGGCGTTCCAGTGGAAGTTGGC
                        TTCGCCAACGAGAAGAGCGCCTACTTTCATGCGGCCACAACGCCCAACACTTTCCTCCGC
                                                                                              --TGACTCTCTGGACCTCGATCCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTC
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Pred. No. 2e-47;
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P-PSDB; AAR97299
                   WPI; 1996-209359/21
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                                                    Le Bourdelles B,
                                                                                                                               01-OCT-1994;
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                                                                                          SHARP & DOHME LTD
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also stably co-transfected eukaryotic cells expressing
ntg. these subunit(s), used for screening and designin
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The invention relates to an isolated mammalian polypeptide (I), which is CC a mutant of gamma-aminobutyric acid (GABA) receptor subunit. The mutation CC disrupts the functioning of an assembled GABA receptor, its functional CC fragment or homologue, and creates a phenotype of epilepsy, anxiety, CC manic depression, phobic obsessive symptoms, Alzheimer's disease, CC schizophrenia, migraine and/or obesity. (I), the polynuclaotide (II) CC encoding (I) and antibody (III) to (I) are useful in the diagnosis of CC epilepsy, anxiety, manic depression, phobic obsessive symptoms, CC Alzheimer's disease, schizophrenia, migraine and/or obesity. (III) is CC useful for treating the above conditions. (I)-(III) are useful in CC screening of candidate pharmaceutical agents, where high-throughput CC conditate gene expression in biological samples. Oligonucleotides or CC quantitate gene expression in biological samples. Oligonucleotides or CC conditions derived from (II) are useful as probes in a microarray CC used to monitor the expression level of large number of genes. (I)-(III) care useful for the study of the function of a GABA receptor, to study the mechanism of the disease as related to GABA receptor, for the creation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; Anticonvulsant; Tranquiliser; Antimanic; Antidepressant; Nootropic; Neuroprotective; Neuroleptic; Antimigraine; Anorectic; gamma-aminobutyric acid receptor subunit; GABA; epilepsy; anxiety manic depression; phobic obsessive symptom; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK27334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mutant gamma-aminobutyric acid receptor subunits and DNA molecule, useful for diagnosing epilepsy, Alzheimer's disease, migraine, obe anxiety, manic depression and schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 schizophrenia; migraine; obesity; receptor; gene; ds.
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11-MAY-2001;
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Matches 484
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CTGGAGTATGC
                                                                                                                           ACCGTGCTCACCATGACCACCCAGAGCTCTGGCTCCCGGGGCCTCTTTGCCTAAGGTGTCC
                                                                                                                                                                                                                                                                                                  ATGAACTTCAAGTCCGCTGGCCAGTTCCCACGGCTCAGCCTGCACCTTCCACCTGCGGAGG
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                                                                                                                                                                                                                                      AACCGCGGCGTGTACATCCATCCCTACATGCCCTCCGTCCTGCTGGTCGCCATGTCC
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                                               GCCATCAAGGCACTGGACGTCTACTTCTGGATCTGCTATGTCTTCGTGTTTGCCGCCCCTG
                                                                           TACGTGAAGGCAATCGACATCTGGATGGCTGTGTGTCTGCTCTTTGTGTTCGCTGCCTTG 104:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and PCR primers of the invention.
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53.1%;
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Pred. No. 9.8e-44;
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RESULT 12
AAD21378
ID AAD21
XX AAD21
XX AAD21
XX AAD21
XX T1ck,
KW T1ck,
KW 11gan
XX T1ck,
KW 11gan
XX T1ck,
KW 11gan
XX AAD20
XX T1ck,
KW 11gan
XX AAD21
XX
                                                                                                                                                                                                                                                                                                       CC Dermancentor variabilis (DV) (American dog tick) ligand gated innocation channel/L-glutamate gated chloride channel (LGC/GluCl) protein.

CC LGIC/GluCl DNA is useful for identifying a compound that modulates

CC glutamate-gated channel protein activity and for identifying a modulator

CC of LGIC/GluCl Channel protein. LGIC/GluCl DNA is used for establishing

CC novel insecticide screens, validate potential lead compounds with

CC insecticidal activity for use in treating parasitic infections in humans

CC or animals, as hybridisation probes to isolate related genes from other

CC organisms to establish additional pesticide drug screens and also used

CC in competition. binding experiments or for functional chloride channel

CC channel. Heterologous expression of LGIC/GluCl protein allows the

CC channel. Heterologous expression of LGIC/GluCl protein active against parasitic

CC invertebrate species relevant to animal and human health, especially in

CC intertebrate species relevant to animal and human health, where the

CC modulators act as effective insecticidal, acaricidal, mitacidal and/or

CC mematocidal treatments for use in animal and human health and/or crop

CC specific disorders. The present sequence is Rhipicephalus sanguineus

CC Genes

CC Control CC Lond I probe which is used for screening Dermacentor LGIC/GluCl 1
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                                                                                                 Matches 466;
                                                                                                                               Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tick; acaricide; mitacide; crop protection; nematocide; insecticide; ligand gated ion channel/L-glutamate gated chloride channel; LGIC/GluCl; parasitic infection; pesticide drug screen; tick infection; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a purified nucleic acid molecule encoding Dermancentor variabilis (Dv) (American dog tick) ligand gated ion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cully DF,
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                                                                                                                                                                                                                             Sequence 1197
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                                                                                                                               Local Similarity
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226 AACATCTTCATCAACAGTTTCAGCTCCGTCACCAAGACCACAATGGACTACCGGGTGAAT 285
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55.0%;
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                                                                                       Score 187.6; DB 2
Pred. No. 3.9e-43;
0; Mismatches 334
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В

AACATCTTTGTAAGAAGTATCGGCAGAATTGATGACGTCACCATGGAGTACACAGTGCAA 156

Gaps

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RESULT 13
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ID AAD22
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AC AAD22
XX
T2-FE
DT 12-FE
XX
XX
GAMMe
KW GABA-
KW GA
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                                                               {\tt GABA}\textsc{-gated} chloride channel; recombinant expression; domestic GluCl DNA; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                   AAD22082 standard;
      Rhipicephalus sanguineus
                                                                                                                            Gamma -aminobutyric acid; GABA; tick infestation; mite; antiparasitic;
                                                                                                                                                                                                   R. sanguineus GluCl DNA probe
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The invention relates to gamma aminobutyric acid (GABA)-gated chloride channels and their corresponding nucleic acid molecules. GABA-gated chloride channel proteins and DNA's are useful for preventing and treating tick infestation, particularly in humans, dogs, cattle, horses, deer, or other wild or domesticated animals. The nucleic acids are useful as hybridisation probes or Polymerase Chain Reaction primers for identifying the presence of Dermacentor variabilis GABA-gated chloride channel nucleic acid or DNA's encoding for a GABA receptor. The nucleic acids are also useful for the recombinant expression of D. variabilis GABA-gated chloride channel proteins exert toxic effects on other ticks or related parasites such as mites. The present sequence is Rhipicephalus sanguineus GluCl DNA probe which is used for cloning Dermacentor variabilis GABA-gated chloride
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200174884-A1
                                                                                                                                                                                                                                                                                                                                                                                 New polypeptide useful for preventing or treating tick infestation, humans, dogs, cattle, horses, deer, or other wild or domesticated animals, comprises the Dermacentor variabilis gamma-aminobutyric aci (GABA)-gated chloride channel -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MERI ) MERCK & CO
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Sequence 1197 BP; 268 A; 358 C; 311 G;
                                             channel DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cully D,
                                                                                                                                                                                                                                                                                                                                              Page 23-24; 59pp;
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                                                                                                                                                                                                                                                                                                                                                  English
          260 T; 0 other;
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Matches Query Match Best Local Similarity 466; Conservative 11.4%; 0; Score 187.6; DB 2 Pred. No. 3.9e-43; Mismatches DB 24; Length 1197; 334; Indels 48;

δõ 20 밁 Š 뫄 δÃ 멍 δÃ Ş В 217 226 AACATCTTCATCAACAGTTTCAGCTCCGTCACCAAGACCACAATGGACTACCGGGTGAAT 285 406 157 277 646 TTTGAGTGGCTGGAAGATGCTCCTGCTGTCCAAGTGGCTGAGGGGGCTGACTCTGCCCCAG 97 AATGAGAAAGGGGCCAACTTCCATGAGGTGACCACGGACAAGATTACTGCGCATCTTC TCTCTGGACCTCGATCCCTCCATGCTGGAACCTCTATCTGGGAAGCCAGACCTCTTCTTTGCT 405 GTCTTCTTGCGGCAACAGTGGAATGACCCACGCCTGTCCTACCGAGAATATCCTGATGAC 345 CTCAAGAACTTCCCCATGGACATCCAGACGTGCACGATGCAGCTTGAGAGCTCATCCATA CCCAACGGCGACGTTCTCTTCAGCATCAGAATATCCTTGGTGCTTTCATGTCCGATGAAC GTTCGCTACCTGACGCTCACCGAACCGGACAAGCTTTGGAAGCCGGACCTGTTTTTCTCC ATGACGTTCAGAGAGCAGTGGCGGGACGACGAGACTCCAGTACGACGACTTGGGCGGCCAG 216 AACATCTTTGTAAGAAGTATCGGCAGAATTGATGACGTCACCATGGAGTACACAGTGCAA 156 AACGAGAAAGAGGGACACTTCCACAACATCATGCCCCAACGTGCTTCTACGCATACAT CTCTGCAGCCCTCTGCCATCTCTGTCACTTTCAGTTGGCTACACCATGAAAGACCTCGTG CTGAAATTTTATCCTTTGGATAAACAAATCTGCTCTATCGTCATGGTGAGCT-------- ATGGGTATACAACAGAGGACCTGGTG 585 465 336 705 645 448 396 525 276 474

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                               Novel L-glutamate-gated chloride channel proteins from Rhipicephalus sanguineus for identifying compounds which modulate the channel proteins, which are useful as insecticides, anthelmintics and
                                                                                                                                                Warmke JW,
                                                                                                                                                                                                              31-MAR-2000;
                                                                                                                                                                                                                                            28-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhipicephalus sanguineus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brown dog tick; glutamate-gated chloride channel; GluCl2; crop protection; insecticide; nematocide; clone Tl2; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R. sanguineus glutamate-gated chloride channel 1 cDNA clone,
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AGCTCTGGCTCCCGGGCCTCTTTGCCTAAGGTGTCCTACGTGAAGGCAATCGACATCTGG
                                                                                                                             ATGTACATCCCCAGCCTACTCATCGTCATCCTGGGTCTCCTTCTGGATCAACATG
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                                                                             GATGCTGCCCCTGCCCGTGTGGGCCTGGGCATCACCACCGTGCTCACCATGACCACCCAG
                                                                                                           ATCTACATCCCGTGCTGCATGCTGGTCATCGTGTCCTGGGTGTCGTTCTGGCTCGACCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brown dog tick; glutamate-gated chloride channel; GluCl1; GluCl2; crop protection; insecticide; nematocide; acaricide; clone T82; ss.
                                                                                                          The invention relates to Rhipicephalus sanguineus (brown dog tick) L-glutamate-gated chloride channel proteins (GluCl1 and GluCl2) and nucleic acid molecules encoding such proteins. GluCl channel proteins are useful for identifying modulators. The compounds identified as modulators are useful for insecticidal, mitacidal and/or nematocidal treatment for use in animal and human health and/or crop protection. The compounds are also useful in screening for and selecting compounds active against parasitic invertebrate species relevant to animal and human health, including worms, fleas, ticks, mites and lice. Heterologous cell lines expressing functional GluCl1 and GluCl2 channel functional forms are useful functional functional of the second control of the second c
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                                                                   for establishing functional or binding assays to identify novel gluCl channel modulators. The present sequence is R. sanguineus
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/note= "This region is specifically referred
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  509 A; 727
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Query Match

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Score 187.6;

DB 22;

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

AX39250 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM Result No. ဂ ဂ ဂ 1521. 1503. 1002. 695.8 659.2 656.2 244. c 239 5 654.8 654.8 654.6 655.0 235. 232. 232. 232. 232. 230. 227. 227. Score AX392950 Sequence 52 AX392950 AX392950.1 Match 40 1874 bp 52 from Patent WO0212340. 1595 100269 657 194822 Length GI:19700997 DВ 10 9 9 5 6 9 5 6 10 10 10 10 HSGLYRA2 RNO310837 RNIGRAA2 DRE404970 RNO310839 AF214575 AF094754 AF094755 AF362764 DRE308517 HS1055C14 E03608 AL671887 BC032635 AF268376 AF488379 DRE404971 AY094975 RNO310838 HSU93917 AY094974 DRES81 HSU33267 RNIGRA1 RNO310836 RNNEOGLY RNO310834 RATGLYRA1 ALIGNMENTS DNA linear AJ310834 Rattus no D00833 Rattus norvegicu S22008 H.sapiens a AF268375 Bos tauru S73718 Glral = inhib AJ310835 Rattus no X55246 R.norvegicu AJ308316 Danio rer AJ005812 Danio rer AJ005812 Danio rer AJ005812 Danio rer AJ005817 Human qlyci AY094975 Morone am Ugagir Morone am Ugagir Morone am Ugagir Morone am AJ310836 Rattus no M55250 Ratinhibit AF488379 Danio rer AL049610 Human DNA E03608 DNA encodin AL671887 Mus muscu AJ308517 Danio rer AL049610 Human DNA E03608 DNA encodin AL671887 Mus muscu AJ308517 Danio rer AL049671 Danio rer AL049671 Danio rer AL049671 Danio rer AJ404971 Danio rer AJ404971 Danio rer X52009 H.sapiens a AJ310837 Rattus no X61159 R.norvegicu X57281 Rat NG1yR m AJ310834 Rattus no AX037570 Sequence 293848 Human DNA s AF018157 Homo sapi X81202 M.musculus AF094754 Homo sapi AF094755 Homo sapi U33267 Human glyci BC032635 Homo sapi AJ404970 Danio rer AX392950 Sequence AX037565 Sequence Description AF268376 Bos tauru AJ310839 Rattus no AF214575 Mus muscu Y00276 R.norvegiuc S73717 GLRA1-inhib AF462147 Mus muscu PAT 23-MAR-2002

REFERENCE

human.

AUTHORS

Yue,H., Thornton,M., Ramkumar,J., Tang,Y.T., Azimzai,Y., Baughn,M.R., Yang,J., Yao,M.G., Lal,P., Walia,N.K., Gandhi,A.R., Hafalia,A.J., Nguyen,D.B., Patterson,C., Elliott,V.S.,

Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.

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Patent: WO 0058461-A 1 05-OCT-2000;

RAPPOLD HOERBRAND GUDRUN (DE)
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AX037565
AX037565.1
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Location/Qualifiers
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1563 1320 1260 1443 1200 1383

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16-NOV-2000

Qy 661 Db 619	Oy 601	Oy 541 Db 541	Oy 481 Db 481	Oy 421 Db 421	Qy 361 Db 361	Qy 301 Db 301	Oy 241 Db 241	Qy 181 Db 181	Qy 121 Db 121	Oy 61 Db 61	Оу	Query Match Best Local Si Matches 1585;	BASE COUNT			CDS	source
1 GATGCTCCTGCTGCCAAGTGGCTGAGGGGCTGACTCTGCCCCAGTTTATCTTGCGGGAT 720	1 CCATCTCTGTCACTTTCAGTTGGCTACACCATGAAAGACCTCGTGTTTTGAGTGGCTGGAA 660 	1 ATGGACATCCAGACGTGCACGATGCAGCTTGAGAGCTCATCCATACTCTGCAGCCCTCTG 600	1 CTGTACAGCATCAGGCTGACCCTCATTTTGTCCTGCCTGATGGACCTCAAGAACTTCCCC 540	1 AACTTCCATGAGGTGACCACGGACAACAAGTTACTGCGCATCTTCAAGAATGGGAATGTG 480	1 CCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCTTTGCTAATGAGAAAGGGGCC 420	1 CAGTGGAATGACCCACGCCTGTCCTACCGAGAATATCCTGATGACTCTCTGGACCTCGAT 360	1 AGTTTCAGCTCCGTCACCAAGACCACAATGGACTACCGGGTGAATGTCTTCTTGCGGCAA 300 	1 AGGATTCGGCCCAATTTTAAAGGCCCACCCGTGAACGTGACCTGCAACATCTTCATCAAC 240	1 CCCATGTCCCCCTCTGATTTCCTAGACAAACTTATGGGGCGAACATCTGGATATGATGCC 180	1 GTCCTCCTCAGGGTGGCCTTGGCAAAAGAGGGAAGTCAAATCTGGAACCAAGGGGTCCCAG 120	TGACAACTCTTGTTCCTGCAACCCTCTCCTTCCTTCTTCTGGACCCTGCCAGGGCAG 60	h Similarity 96.6%; Pred. No. 0; 85; Conservative 0; Mismatches 12; Indels 44; Gaps. 3;	EYAAINFYSRQHKEFIRLRRQRRQRLEEDIIQESRFYFRGYGLGHCLQARDGGPMEG SGIYSPQPPAPLLRGGETTRKLYVD" 378 a 440 c 379 g 403 t	NDPRLSYREYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNV LYSIRUTLILSCLMDLKNEPMDIOTCTMOLERFGYRMKDLVFEMLEDAPAVQVARSCLT LPQFILRDEKDLGCCTKHYNTGKTFCIEVKFHLERQMGYYLJQMYIPSLLIVILSMVS FWILNDDAFDARVGLGITTVLTMTTQSSGSRASLEKVSYVKAIDIWAAVCLLFVFAALL	/protein_id="CAC16495.1" /db_xref="G1:11226997" /translation="mTTLYPATLSFLLLWTLPGQVLLRVALAKEEVKSGTKGSQPMSP SDFLDKLMGRTSGYDARIRPNFKGPPVNVTCNIFINSFSSITKTTMDYRVNVFLROOW	11254 /note="unnamed protein product" /codon_start=1 /trans1_table=11	<pre>11600 /organism="synthetic construct" /db_xref="taxon:32630" /note="cDNA"</pre>
ACCESSION VERSION KEYWORDS	RESULT 3 AF462147 LOCUS	Db	DЬ	d d	ОУ	Db Db	oy Db	Qy	ОУ	Qy Db.	Дb	Qу	Фр	Qy	Qy Db	рь	Qy
complete cds. AF462147.1 GI:18448710	AF462147 1251 bp mrNA linear N Mus musculus diveine receptor alba d subusit (Clad	1520 CTAAAAAAAAAAAAAAA 1640 	TGTGGGCCTATATTGCATGGTG	GGTTTGGACAGTTCCTTCCTGATCTCCCACTCACACTTCAACTACCACTCCCAAAGCTA	1440 TGCTGCTGGCCTCCTGCTTCCTCCTGGGTGGGCTTTCTCCCTCAGTTAGACTCCATTAGG 1499	1380 AGTGCTATGGTCAGAAGATATCCACCAGGCTCTGTGAATAGGGTGGGAGCTATAGAGTCC 1439 . 	C-GGGCTGTCTTCCCTTTTCCTCATCTTCAATATCTTCTACTGGGTTGTCTATAA C-II	1261 GAAGGAGAAACCCACGCGGAAACTCTACGTGGACTGAGCCAAGAGAATTGACACCATCTCC 1320 	1201 GGAGGTCCAATGGAAGGTTCTGGCATTTATAGTCCCCAACCTCCAGCCCCTCTTCTAAGG 1260	1141 CAAGAAAGTCGTTTCTARTTCCCTGGCTATGGCCTAGGCCACTGCCTCCAGGCAAGACAT 1200 	AAAGAATTCATACGACTTCGAAGAAGGCAGAGGCGCCAACGCTTGGAGGAAGATATCATC 1	1021 CTCTTTGTGTTCGCTGCCTTGCTGGAGTATGCTGCCATAAATTTTGTTTCTCGTCAGCAT 1080	961 GCCTCTTTGCCTAAGGTGTCCTACGTGAAGGCAATCGACATCTGGATGGCTGTGTGTG	901 CGTGTGGGCCTGGGCATCACCACCGTGCTCACCATGACCACCAGAGCTCTGGCTCCCGG 960 	841 CTACTCATCGTCATCCTGTCCTGGGTCTCCTTCTGGATCAACATGGATGCTGCCCCTGCC 900 	781 GTAAAGTTTCACCTGGAACGGCAGATGGGCTACTATCTGATTCAGATGTACATCCCCAGC 840	

Qy 364 TCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTTGCTAATGAGAAAGGGGCCAAC 423	184 61 244 121 304 181	Query Match 61.1%; Score 1002.2; DB 10; Length 1251; Best Local Similarity 87.2%; Pred. No. 8.9e-268; Matches 1128; Conservative 0; Mismatches 123; Indels 42; Gaps 1; Qy 124 ATGTCCCCCTCTGATTTCCTAGACAAACTTATGGGGCGAACATCTGGATATGATGCCAGG 183	/PROTEIN_1d="ALLG9899.1" //db_xref="G1:18448711" //db_xref="G1:18448711" //db_xref="G1:18448711" //db_xref="MSPSDFLbLMGRTSGYDARIRPNEKGPPVNVTCNIFINSFGSV //ETTMDKRVNVFLRQQWNDPRLAYREYPDDSLDLNPSMLESIWKPDLFFANEKGANFH EVTTDNKLLRIFKNGNVLYSIRLTLILSCPMDLKNFPMDIQTCTMQLESFGYTMNDLM FEWLEDAPAVQVAEGLTLPQFILRDEKDLGYCTKHYNTGKFTG1EVKFHLERQMGYYL FEWLEDAPAVQVAEGLTLPQFILRDEKDLGYCTKHYNTGKFTG1EVKFHLERQMGYYL IQMYIPSLLIVILSWYSFWINMDAAPARVGLGITTVLTMTTTQSSGRASLPKVSYVKA IQMYIPSLLIVILSWYSFWINMDAAPARVGLGITTVLTMTTTQSSGRASLPKVSYVKA IQMYIPSLLIVILSWYSFWINMSAAPARVGLGITTVLTMTTTQSSGRASLPKVSYVKA IQMYIPSLLIVILSWYSFWINMSAAPARVGLGTTVLTRATTQSSGRASLPKVSYVKA IDMAVCLLFVFAALLEYAAVNFYSRQHKEEMTLRRQRRQMEDJIRESRFYFRG YGLGHCLQARDGGPMEGSSIYSPQPFTPLLKEGETWRKLYVDRAKRIDTISRAVFPFT BASE COUNT 324 a 314 c 281 g 332 t ORRIGIN	gene 11251 //gene="Glra4" /note="mmGlra4" CDS 11251 /gene="Glra4" /note="ligand-gated ion channel" /codon_start=1 /codon_drafter receptor alpha 4 subunit"	FEATURES Location/Qualificiers 1. 1251 Source Jorganism="Mus musculus" /strain="B6C3/Fe" /db_xref="taxon:10090" /chromosome="N" /tissue_type="spinal cord"		rtebrata; Eut; ; Muridae; Mi
RESULT 4 DRE404970 LOCUS DDEFINITION DDEFINITION Danio rerio mRNA for glycine receptor alphaZ2 subunit (glyR alpha Queen alpha yearsion VERSION AJ404970 AJ404970 AJ404970 AJ404970 AJ404970 SOURCE SOURCE Cebrafish. ORGANISM Danio rerio Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		Qy 1144 GAAAGTCGTTTCTATTTCCGTGGCTATGGCTTGGGCCACTGCCAGGCAAGAGATGGA 1203	Qy 964 TCTTTGCCTAAGGTGTCCTACGTGAAGGCAATCGACATCTGGATGGCTGTGTCTCCTC 1023	Qy 844 CTCATCGTCATCCTGCTCGGGTCTCCTGGATCAACATGGATGCTGCCCCTGCCCGT 903	OY ANGELIC PROCED TO THE ANGEL RELABORATION CONTROL TO ANGEL RELABORATION CONTROL TO A CONTRO	455TIGGCTACACCATGATTACTCCAATTTATTTTCCGGGATGAC	Oy 544 GACATCCAGACGTGCACGATGCAGCTTGAGAGCTCATCCATACTCTGCAGCCCTCTGCCA 603

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JOURNAL
REFERENCE
AUTHORS
TITLE
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Best Local Similarity
Matches 949; Conserv
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Submitted (18-JUL-2000) Goblet C., Biotechnologies, Institut
Pasteur, 25 rue du Dr Roux, 75724-Paris Cedex 15, FRANCE
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 2045)
Imboden,M., de Saint Jan,D., Leulier,F., Korn,H., Gob Bregestovski,P.
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                                                                                                                                                                                                                                                                                                                                                                                                   AGCCCATGTCCCCCTCTGATTTCCTAGACAACTTATGGGGCGAACATCTGGATATGATG
CCAACTTCCATGAGGTGACCACGGACAACAAGTTACTGCGCATCTTCAAGAATGGGAATG
                                                                                                                                                  ACCCTTCTATGTTGGACTCCATATGGAAACCTGACTTGTTTTTTGCTAATGAGAAAGGTG
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/product="glycine receptor alphaZ2 subunit"
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/protein_id="CAC1687.1"
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DFLDKLMGRTSGYDARIRENFKGPPVNVTCNIFINSFGSITETHMDYRLNVFLKQOWN
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DPLDKLMGRTSGYDASLDLDPSMLDSIMKPDLFFAREKGANEHEVTTDNKLLFIFONGNVL
DPLLAYSEYDASLDLDPSMLDSIMKPDLFFAREKGYTHNDLIFEWISDNPVQVADDLTLF
VSIRLTLILSCPMDLKNFPMDIQTCTMQLESFGYTHNDLIFEWISDNPVQVADDLTLF
OFVLKEEKDLGYCTKHYMTGKFTGIEVKFHLEROMGYTLIOMYLPSLLVILSWVSFW
INMDAPARYGLGITTYLTMTTOSSGSRASLFEVSYVVAIDIWAVCLLIVFAALLEV
INMDAPARYGLGITTYLTMTTOSSGSRASLFEVSYVVAIDIWAVCLLIVFAALLEV
ANVNFVSROHKEFIRLRKKORRORIEEDLYRESRGFYFRGYGLGHCLQTKDGTAVEGS
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/gene="glyR alpha"
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/tissue_type="brain"
/dev_stage="adult"
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Rattus norvegicus
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Mammalia; E
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Submitted (14-JUL-1987) Gundelfinger
S82, D-6900 Heidelberg, FRG
2 (bases 1 to 138)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source: strain=Wistar; tissue=Spinal cord; source: clones=GR1, GR6, GR1-6, GR1-6-1; Data kindly reviewed (26-SEP-1987) by Gund
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Grenningloh,G., Rienitz,A., Schmitt,B., Methfessel,C., Beyreuther,K., Gundelfinger,E.D. and Betz,H.
The strychnine-binding subunit of the glycine receptor homology with nicottnic acetylcholine receptors of the glycine receptors 28 (6127), 215-220 (1987)
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                                              GAGAATATCCTGATGACTCTCTGGACCTCGATCCCTTCCATGCTGGACTCTATCTGGAAGC
                                                                                      CCGTGAACGTGACCTGCAACATCTTCATCAACAGTTTCAGCTCCGTCACCAAGACCACAA
CAGACCTCTTCTTTGCTAATGAGAAAGGGGCCAACTTCCATGAGGTGACCACGGACAACA
                                                                                                                                                    CTGTGAACGTGAGTTGCAACATCTTCATCAACAGCTTTGGTTCTATCGCCGAGACAACCA
                                                                                                                                                                                                               AACTTATGGGGGGAACATCTGGATATGATGCCAGGATTCGGCCCAATTTTAAAGGCCCAC
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/translation="SKEVDAARSAPKRMSPSDFLDKLMGRTSGYDARTRPNFKGPPVN
/translation="SKEVDAARSAPKRMSPSDFLDKLMGRTSGYDARTRPNFKGPPVN
VSCNIFINSFGSISETTMDYRVNIFLRQQWNDPRLAYNEYPDDSLDLDPSMLDSIWKP
DLFFANEKGAHFHEITTDNKLLRISRNGNVLYSIRITLTLACPMDLKNFPMIVQTCIM
QLESFGYTMNDLIFEWQEQGAVQVADGLTLPQFILKEEKDLRYCTKHYNTGKFTCIEA
RFHLERQMGYYLIQMYIPSLLIVILSWISFWINMDAAPARVGLGTTYVLTMTTQSSGS
RASLERVSYVKAIDIWMAVCLLFVFSALLEYAAVNFVSRQHKELLRFRKRRHKDDE
GGEGRENFSAYGMGPACLQAKDGISVKGANNNNTTNPAAPAPSKSPEEMRKLFIQRAKK
LDKISRIGFPMAFLIFNMFYWIIYKIVRREDVHNK"
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387 c 361 g
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561
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/product="glycine receptor strychnine binding
/protein_id="CAA68378.1"
/db_xref="GI:755778"
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<1. .1286</pre>
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Rodentia;
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Pred. No. 3.3e-172;
0; Mismatches 313;
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                                                                                                     TCTACGTGGACTGAGCCAAGAGAATTGACACCATCTCCCGGGCTGTCTTCCCTTTCACTT
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                                                                                                                                     TCCTCATCTTCAATATCTTCTACTGGGTTGTCTATAAAGTGCTATGGTCAGAAGATATCC 1402
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0у 35	Qy 29 Db 33	Qy 236 Db 275	Oy · 176	Qy 116 Db 155	Query Match Best Local Matches 94	BASE COUNT				CDS	gene	FEATURES source		TITLE JOURNAL MEDLINE	REFERENCE AUTHORS	KEYWORDS SOURCE ORGANISM	z o	S73717 LOCUS
TCGATCCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCTTTGCTAATGAGAAAG 415	96 GGCAACAGTGGAATGACCCACGCCTGTCCTACCGAGAATATCCTGATGACTCTCTGGACC 355	6 TCAACAGTTTCAGCTCCGTCACCAAGACCACAATGGACTACCGGGTGAATGTCTTCTTGC 295	76 ATGCCAGGATTCGGCCCAATTTTAAAGGCCCACCCGTGAACGTGACCTGCAACATCTTCA 235	CCCAGCCCATGTCCCCCTCTGATTTCCTAGACAAACTTATGGGGGGGAACATCTGGATATG 17	ch 40.0%; Score 656.2; DB 10; Length 1407; 1 Similarity 72.6%; Pred. No. 2.2e-171; 942; Conservative : 0; Mismatches 298; Indels 57; Gaps 5;	PPPAPSKSPEEMRKLFIQRAKKIDKISRIGFPMAFLIFNMFYWIIYKIVRREDVHNK" 349 a 404 c 332 g 322 t	YNEYPDDSLDLDPSMLDSJWKPDLFFANEKGAHFREITTDNKLLRISRNGNYLYSIRI TLTLACPMDLKNFPMDVQTCIMQLESFGYTMNDLIFEWQEQGAVQVADGLTLPQFILK EEKDLRYCTKHYNTGKFTCIEARFHLERQMGYYLIQMYIPSLLIVILSMISFWINMDA APARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLFVFSALLEYAAVNF	/protein_id="AAB32157.2" /db_xref="GI:9247215" /translation="MYSFNTLRFYLWETIVEFSLAASKEAEAARSAPKPMSPSDFLDK LMGRTSGYDARIRPNFKGPPVNVSCNIFINSFGSIAETTMDYRVNIFLROOWNDPRLA	<pre>published reference; GLRA1 protein; GlyR alpha 1" /codon_start=1 /product="inhibitory glycine receptor alpha 1 subunit short form"</pre>	<pre>581407 /gene="0lral" /note="alternatively spliced; This sequence comes from /note="alternatively spliced; This sequence comes from Fig2a; conceptual translation differs from that in</pre>	<pre>/tissue_type="brainstem and spinal cord" /note="A)HeJ" 1. 1407 /gene="GIral"</pre>	<pre>cation/Qualifiers .1407 rganism="Mus sp." b_xref="taxon:10095</pre>	7920629 GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 156492] from the original journal article. This sequence comes from Fig. 2a.	mutation in the gene encoding the alpha 1 subunit of t glycine receptor in the spasmodic mouse 7 (2), 131-135 (1994)	Sutheria; Rodentia; Sciurognathi; Muridae, to 1407) Buckwalter,M.S., Lynch,J.W., Handford,C., Wasmuth,J.J., Camper,S.A., Schoffield,P.,	Mus sp. Mus sp. Eukarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	<pre>LRA1=inhibitory glycine receptor alpha 1 subunit [m rainstem, spinal cord, mRNA, 1407 nt]. 73717 73717.1 GI:765206</pre>	mRNA linear ROD 1
RESULT 7 HSGLYRA2	Db Qy	Ду Дь	Db Oy	Оу	Оy	Ωy	Qy db	Оу	Qу	Qу	Оу	Qу	Qy Db	Qy Db	Qy Db	Оy	Qу	οь
7	1370 TTGTCTATAAAGTGCTATGGTCAGAAGATATCCACCA 1406 	1310 ACACCARCTCCCGGGCTGTTCCCTTTCACTTTCCTCARCTTCCATATATCTTCTACTGGG 1369 111			1136 TCATCCAAGAAGTCGTTTCTATTTCCGTGGCTATGGCTTGGGCCACTGCCTGCAGG 1192	1076 AGCATAAAGAATTCATACGACTTCGAAGAAGGCAGAGGCCGCAACGCTTGGAGGAAGATA 1135	GTCTGCTCTTTGTGTTCGCTGCCTTGCTGGAGTATGCTGCCATAAATTTTGTTTCTCGTC	956 CCCGGGCCTCTTTGCCTAAGGTGTCCTACGTGAAGGCAATCGACATCTGGATGGCTGTGT 1015	896 CTGCCCGTGTGGGCCTGGGCATCACCACCGTGCTCACCATGACCACCCAGAGCTCTGGCT 955	836 CCAGCCTACTCATCCTCATCCTGTCCTGGGTCTCCTTCTGGATCAACATGGATGCTGCCC 895	776 TCGAGGTAAAGTTTCACCTGGAACGGCAGATGGGCTACTATCTGATTCAGATGTACATCC 835	716 GGGATGAGAAGGATCTAGGCTGTTGTACCAAGCACTACAACACAGGGAAATTCACCTGCA 775	656 TGGAAGATGCTCCTGCTGTCCAAGTGGCTGAGGGGCTGACTCTGCCCCAGTTTATCTTGC 715	596 CTCTGCCATCTCTGTCACTTTCAGTTGGCTACACCATGAAAGACCTCGTGTTTGAGTGGC 655	536 TCCCCATGGACATCCAGACGTGCACGATGCAGCCTTGAGAGCCTCATCCATACTCTGCAGCC 595	476 ATGTGCTGTACAGCATCAGGCTGACCCTCATTTTGTCCTGCCTG	GGGCCACTTCCATGAGGTGACCACGGACAACAAGTTACTGCGCATCTTCAAGAATGGA	TTGACCCATCTATGTTGGATTCCATCTGGAAGCCTGACTTGTTCTTTGCCAATGAGAAGG

329 GAGAATATCCTGATGACTCTCTGGACCTCGATCCCTCCATGCTGGACTCTATCTGGAAGC		Oy 149 AACTTATGGGGCGAACATCTGGATATGATGCCAGGATTCGGCCCAATTTTAAAGGCCCAC 208	89 AGGAAGTCAAATCTGGAACCAAGGGGTCCCAGCCCATGTCCCCCCTCTGATTTCCTAGACA 14	Query Match 40.0%; Score 656; DB 9; Length 1715; Best Local Similarity 71.9%; Pred. No. 2.6e-171; Matches 952; Conservative 0; Mismatches 315; Indels 57; Gaps 5;	VSRQHKELLRERRKRIHKEDDAGGERFINSAYEGKAGACIQAKDGISYKGANISHTIN PPPAPSKSPEEMRKLEIQRAKKIDKISRIGEPMAPLIENMFYWIIYKIVRREDVHNQ" BASE COUNT 424 a 480 c 407 g 404 t ORIGIN	YNEYPDDSLDLDSSINDSTWKPDLFEANEKGAHTHEITTIJKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	/db_xref="G1:31851" /db_xref="SWISS-PROT: P23415" /db_xref="SWISS-PROT: P23415" /translation="MXSRWTLRLYLSGAIVFFSLAASKEAEAARSATKPMSPSDFLDK /MCRTSKYDARIRENFKGPPVNVSCUTFTNSFGSTAFTTWADYRVATFIROOMNDDFLA	/note="strychnine binding alpha-1 subunit" /codon_start=1 /product="inhibitory glycine.receptor" /protein id="raa18558 1"	gene 2971646 /gene="GLYRA2" CDS 2971646 /gene="GLYRA2"	/chromoseme="X" /chromoseme="X" /map="Xp21.2-p22.1" /tissue_Type="brain" /dev stage="fetal"	FEATURES Location/Qualifiers Source 1. 1715 //organism="Homo sapiens" //dh yref="++xyon.qs/06"		AUTHORS Grenningloh,G., Schmieden,V., Schofield,P.R., Seeburg,P.H., Siddique,T., Mohandas,T.K., Becker,C.M. and Betz,H. TITLE Alpha subunit variants of the human glycine receptor: primary structures, functional expression and chromosomal localization of	ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo REFERENCE 1 (bases 1 to 1715)	ACCESSION X52009 VERSION X52009.1 GI:31850 KEYWORDS 91ycine receptor; inhibitory glycine receptor; strychnine binding. SOURCE Homo saniens	LOCUS HSGLYRA2 1715 bp mRNA linear PRI 28-MAY-1993 DEFINITION H.sapiens alpha-1 strychnine binding subunit of inhibitory glycine
Qy 1403 ACCA 1406 Db 1636 ACAA 1639 RESULT 8	Db 1516 TCTTCATCCAGAGGGCCAÁGAAGATCGACÁAAATATCCCGCATTGGCTTCCCCATGGCCT 1575 Oy 1343 TCCTCATCTTCAATATCTTCTACTGGGTTGTCTATAAAGTGCTCATGTCCAGAAGATATCC 1402	QY 1223 GCATTTATAGTCCCCACCTCCTCTAGGGAAGGAAACCACGCGGAAAC 1282	1169 ATGGCTTGGGCCACTGCCTGCAGGCAAGAGATGGAGGTCCAATGGAAGGTTCTG	QY 1109 AGAGGCGCCAACGCTTGGAGGAAGATATCATCCAAGAAAGTCGTTTCTATTTCCGTGGCT 1168	QY 1049 ATGCTGCCATAAAATTTTGTTTCTCGTCAGCATAAAGAATTCATACGACTTCGAAGAAGGC 1108	Qy 989 AGGCAATCGACATCTGGATGGCTGTGTGTCTCGCTTGTGTTCGCCTGCCT	Qy 929 TCACCATGACCACCCAGAGCTCTGGCTCCCGGGCCTCTTTGCCTAAGGTGTCCTACGTGA 988	Qy 869 CCTTCTGGATCAACATGGATGCTGCCCCTTGCCCGTTGTGGGCCTTGGGCATCACCACCGTGC 928	Qy 809 GCTACTATCTGATTCAGATGTACATCCCCAGCCTACTCATCGTCATCCTGGGTCT 868	QY 749 ACTACAACAGAGGAAATTCACCTGCATCGAGGTAAAAGTTTCACCTGGAACGGCAGATGG 808	Qy 689 GGCTGACTCTGCCCCAGTTTATCTTGCGGGATGAGAAGGATCTAGGCTGTTGTACCAAGC 748	Qy 629 CCATGAAAGACCTCGTGTTTGAGTGGCTGGAAGATGCTCCTGCTGTCCAAGTGGCTGAGG 688	Qy 569 TTGAGAGCTCATCCATACTCTGCAGCCCTCTGCCATCTCTGTCACTTTCAGTTGGCTACA 628	Qy 509 TGTCCTGCCTGATGGACCTCAAGAACTTCCCCATGGACATCCAGACGTGCACGATGCAGC 568	QY 449 AGTTACTGCGCATCTTCAAGAATGGGAATGTGCTGTACAGCATCAGGCTGACCCTCATTT 508	Db 667 CTGACCTGTTCTTTGCCAACGAGAAGGGGGCCCACTTCCATGAGATCACCACAGAGAACA 726

	CDS CDS BASE COUNT ORIGIN	RNO310837 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE
ABACANACTTATAGGACATCATCTTCATCAACAGTTTTCAGCACAGGATTCAGAAC CCCACCGTGAACTTACCGAACATCTTCAACATTTTATCAACAGTTTTGGAATCAACGCTGTAAACGAACAGTTTTCTTATCAACAGGAATGAACCAACGTTACCGAACATTTTTCTGAACAACATCAACATGAACAACATCAACATCAACAACATTTTCAACAGAACAACATCAACATAACAACAACAACAACAACAACAACAA	/org /str /db /db /db /clc /db /clc /clc /clc /clc /cr /prc /prc /prc /prc /prc /prc /prc	RNO310837 Rattus norvegicus mRNA for glycine receptor alpha 2 precursor. AJ310837 A
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1104 AAGGCAGAGGCGCCAACGCTTGGAGGAAGATATCATCCAAGAAAGTCGTTTCCG 1163	744 CAAGCACTACAACACAGGGAAATTCACCTGCATCGAGGTAAAGTTTCACCTGGAACGGCA 803	384 GAAGCCAGACCTCTTCCTTTGCCTAATGAGAAAGGGGCCAACTTCCATGAGGTGACCACGGA 443 384 GAAACCAGATTTGTTCTTTGCCAATGAGAAAGGAGCCAATTTCCATGATGTCACCACGA 443 384 CAACAAGTTACTTGCTCTTTGCCAATGAGAAAGGAGCCAATTTCCATGATGTCACCACCACCACCACCACCACCACCACCACCACCACCAC

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PQFILKERELGYCTKHYNTGKFTCIFVKFHLERQMGYYLIQWIPSLLIVILSWVSF
WINNDAAPARVALGITTYLTMYTGSSGSRASLFKVSYVKAIDIWMAVCLLFVEAALLE
YAAVNFVSRQHKEFLRLRRRQKRQNKEEDVTRBSRFNNFSGYGWGHCLQVKDGTAVKAT
PANPLPQPPKDADAIKKKFVDRAKRIDTISRAAFPLAFLIFNIFYWITYKIIRHEDVH
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/db_xref="taxon:10116"
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glycine receptor; NG1

Rattus norvegicus.

Rattus norvegicus

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WINNDAAPARVALGITTVLTMTTQSSGSRASLPKVSYVKAIDIMMAVCLLEVFAALLE
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TRANPLPQPPKDADAIKKFVDRAKRIDTISRAAFFLAFLIFNIFYMITYKIIRHEDVH
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/codon_start=1
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/tissue_type="spinal cord"
/dev_stage="10 days old"
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Ouery Mai Best Loca Matches Oy Db Oy Db	CDS	TITLE JOURNAL MEDLINE REFERENCE AUTHORS TITLE JOURNAL COMMENT FEATURES SOURCE	RESULT 11 RN0310834 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE
y Match Local Similarity 72.6%; Pred. No. 6.2e-171; Local Similarity 72.6%; Pred. No. 6.2e-171; hes 941; Conservative 0; Mismatches 299; Indels 57; Gaps 5; 116 CCCAGCCCATGTCCCCCTCGAATTTCCTAGACAACTTATGGGGCGAACATCTGGATATG 175	/Gryantsmi Action (Drey males) /Strain="Spraque-Dawley males" /tisue_type="whole brain" /clone_lib="rat brain marathon-ready cDNA" /clone_lib="rat brain marathon-ready cDNA" /dev_stage="8-12 weeks" 11350 /function="10n channel" /note="alternative splicing, primary transcript" /codon_start=1 /codon_start=1 /product="glycine receptor alpha 1 precursor" /product="glycine receptor alpha 1	openings of the rat recombinant as a function of the number of ag J. Gen. Physiol. 119 (5), 443-466 (2197776) (bases 1 to 1350) Groot-Kormelink, P.J. Direct Submitssion submitted (30-MAR-2001) Groot-Korpharmacology, The School of Pharm London, WCIN 1AX, UNITED KINGDOM related splice variants AJ310835 Location/Qualifiers	mRNA linear ROD 15-AU ine receptor alpha 1 precursor eceptor alpha 1 precursor. eraniata; Vertebrata; Euteleost ciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Grenningloh, G., Beyreuther, K., (
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glycine receptor alpha 1; GlyRalpha1.
Rattus norvegicus (strain:Wistar) older than
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Mammalia; Eutheria;
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269. .1531
                                                                                                                                                                                                                                                                                                                          /product="glycine receptor alpha 1 precursor"
/protein_id="BAA00707.1"
/protein_id="BAA00707.1"
/db_xref="G1:220751"
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YNEYPDDSLDLDPSMLDSIWKPDLFFANEKGAHFHEITTDNKLLRISRNGNVLYSIRI
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593 c 527 g 469 t
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PAPAPSKSPEEMRKLFIQRAKKIDKISRIGFPMAFLIFNMFYWIIYKIVRREDVHNK"
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EEKOLRYCTKHYNTGKFTCIEARFHLERQMGYYLIQMYIPSLLIVILSWISFWINMDA
APARVGLGITTVLTWTTQSSGSRASLPKVSYYKAIDIMMAVCLLFVFSALLEYAAVNF
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/tissue_type="spinal cc
/dev_stage="older than
/note="314 bp upstream
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 CCAAGGATGGCATCTCTGTCAAGGGTGCCAACAACAACAACACCAC
                                   CAAGAGATGGAGGTCCAATGGAAGGTTCTGGCATTTATAGTCCCCAACCTC
                                                                                                                                                                        AGCATAAAGAATTCATACGACTTCGAAGAAGGCAGAGGCGCCCAACGCTTGGAGGAAGATA
                                                                                                                                                                                                          GCCTGCTCTTCGTGTTCTCGGCCCTGCTGGAATATGCCGCTGTCAACTTTGTGTCCCGGC
                                                                                                                                                                                                                            GTCTGCTCTTTGTGTTCGCTGCCTTGCTGGAGTATGCTGCCATAAATTTTGTTTCTCGTC
                                                                                                                                                                                                                                                                              CCCGAGCCTCCCTACCCAAGGTGTCCTACGTGAAAGCTATTGACATCTGGATGGCTGTTT
                                                                                                                                                                                                                                                                                              CCCGGGCCTCTTTGCCTAAGGTGTCCTACGTGAAGGCAATCGACATCTGGATGGCTGTGT
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                                                                     TCATCCAAGAAAGTCGTTTCTATTTCCGTGGCTATGGCTTGGGCC---ACTGCCTGCAGG
                                                                                                                                        AACACAAGGAACTC-----CTTCGATTTAGGAGGAAGCGGCGACATCACAAGGATGATG
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Qy Вb

510 CCTATCTCCTTCAGATTTCTTGGACAAGTTAATGGGAAA

Query Match Query Match Best Local Similarity 70.1%; Pred. No. 1.1e-169; Best Local Similarity 70.1%; Pred. No. 1.1e-169; Best Local Similarity 70.1%; Pred. No. 1.1e-169; Matches 943; Conservative 0; Mismatches 348; Indels 54; Gaps 3; Qy 63 CCTCCTCAGGGCTGGCCATGGCAAAGAGGAAGTCAAATCTGGAACCAAGGGTCCCAGGC 122 Qy 11	NUSERLAYSE PODSELDESMEDS INFROME FOR THE TOP TO THE FORCE OF THE FORCE	CDS 388. 1746 /gene="GLYRAI" /note="strychnine binding alpha-2 subunit" /codon_start=1 /product="inhibitory glycine receptor" /protein_id="GAA3657.1" /db_xref="GI:31849" /db_xref="GI:31849" /db_xref="GH:31849" /db_xref="GH:31	/organism="Homo sapiens" /db_xref="taxon:9606" /tissue_type="brain" /dev_stage="fetal" gene 388. 1746	33975 3780 Location/Qualifiers 11857	Eutheria; Primates; Catarrhini; Hominidae; 1 to 1857) oh.G., Schmieden,V., Schofield,P.R., Seebus T., Mohandas,T.K., Becker,C.M. and Betz,H. unit variants of the human glycine receptous; functional expression and chromosomal lessponding genes	DEFINITION H. Sapiens alpha-2 strychnine binding subunit of initializing given receptor mRNA. ACCESSION X52008	370 TTGTCTATAAGTGCTATGGTCGAAGATATCCACCA 1406 1	1252CTTCTAAGGGAAGGAGAAACCACGCGGAAACTCTAC
Qy 1083 AGAATTCATACGACTTCGAAGAGGCAGAGGCCCAACGCTTGGAGGAAGATATCATCCA 1142	Qy 963 CTCTTTGCCTAAGGTGTCCTACGTGAAGCCAATCGACATCTGGATGGCTGTGTGTCTGCT 1022	Db 1125 CAAGTTTCACCTGGAACGCCAAATGGGATATTATTTGATCCAGATGTACATCCCAAGCCT 1184 Qy 843 ACTCATCGTCATCCTGTCCTGGGTCTCCTTCTGGATCAACATGTACATCCCAAGCCT 1184 Qy 11	Qy 723 GAAGGATCTAGGCTGTTGTACCAAGCACTACAACACAGGGAAATTCACCTGCATCGAGGT 782	Db 965TTGGGTACACGATGAATGACCTGATATTTGAGTGATGA 100/ Qy 663 TGCTCCTGCTGCCCAAGTGGCTGAGGGGCTGACTCTGCCCCAGTTTATCTTGCGGGATGA 722	543 GGACATCCAGACGTG 930 GGATGTCCAGACCTG 603 ATCTCTGTCACTTTC	Qy 423 CTTCCATGAGGTGACCACGGACAACAAGTTACTGCGCATCTTCAAGAATGTGCT 482	OY 303 GTGGAATGACCCACGCCTGTCCTACCGAGAATATCCCTGATGACTCT	OY 183 GATTCGGCCCAATTTTAAAGGCCCACCGTGAACGTGACCC QY 183 GATTCGGCCCAATTTTAAAGGCCCACCGTGAACGTGACCC

QY 1151 GTTTCTATTTCCGTGGCTATGGCTTGGGCCACTGCCTGCAGGCAAGAGATGGAGGTC 1207	89 AGGAAGTCAAATCTGGAACCAAGGGGTCCCAGCCCATGTCCCCCTCTGATTTCCTAGACA 14
Qy 1109 AGAGGCGCC	Query Match 39.4%; Score 646.8; DB 4; Length 1744; Best Local Similarity 71.2%; Pred. No. 9.6e-169; Matches 956; Conservative 0; Mismatches 317; Indels 69; Gaps 5;
OY 1049 ATGCTGCCATAAATTTTGTTTCCGTCAGCATAAAGAATTCATACGACTTCGAAGAAGGC 1108	ANNSNTTNPPPAPSKSPEEMRKLFIQRAKKIDKISRIGFPMAFLIFNMFYWIIYKIVR BASE COUNT 396 a 508 c 451 g 389 t ORIGIN
Qy 989 AGGCAATCGACATCTGGATGGCTGTGTGTCTCTTTTGTGTTTCGCTGCCTTGCTGGAGT 1048	TLTLACPMDLKNFPMDVQTCIMQLESFGYTMNDLIFEWQEGGAVQVADGLTLPQFILK EEKDLRYCTKHYNTGKFTGLEARFHLERQMGYYLLIQMYIPSLLIVILSWISFWINMDA APARVGLGITTVLTMTTQSSGSRASLFKVSYVKAIDIWMAVGLLFVFSALLEYAAVUNF VSRQHKELLFFRKKRRHHKSPMLNLFODDEAGGERFUNFSAVGLGAKDGISVKG
Qy 929 TCACCATGACCACCCAGAGCTCTGGCTCCCGGGCCTCTTTGCCTAAGGTGTCCTACGTGA 988	/db_xref="GI:10180959" /translation="Mysewirizumetivefslaaskeaeaarsaskpmspsdeflok /translation="Mysewirizumetivefslaaskeaeaarsaskpmspsdeflok LMGRTGSYDARIRPNEKGPPVNVSCNIFINSEGSIAETTMDYRVNIFLRQQWNDPRLA YNEYPDDSLDLDPSMLDSTWKPDLFFANEKGAHFHEITTDNKLLRISRNGAVLYSIRI YNEYPDDSLDLDPSMLDSTWKPDLFFANEKGAHFHEITTDNKLLRISRNGAVLYSIRI
Qy 869 CCTTCTGGATCAACATGGATGCTGCCCCTGCCCGTGTGGGCCTGGGCATCACCACCGTGC 928	
Qy 809 GCTACTATCTGATTCAGATGTACATCCCCAGCCTACTCATCCTCATCCTGTCCTGGGTCT 868	gene 11744 /gene="GIral" CDS 2291602 /gene="GIral"
OY 749 ACTACAACACAGGGAAATTCACCTGCATCGAGGTAAAGTTTCACCTGGAACGGCAGATGG 808	
Qy 689 GCCTGACTCTGCCCCAGTTTATCTTGCGGATGAGAAGGATCTAGGCTGTTGTACCAAGC 748	nd Schoffeld,P.R. ssion 7-MAY-2000) Neurobiology Program, Ga arch, 384 Victoria Street, Sydney, N
Oy 629 CCATGAAAGACCTCGTGTTTGAGTGGCTGGAAGATGCTCCTGCTGTCCAAGTGGCTGAGG 688	
Qy 569 TTGAGAGCTCATCCATACTCTGCAGCCCTCTGCCATCTCTGTCACTTTCAGTTGGCTACA 628	Healy, P.J. and Schofield, P.R. A nonsense mutation in the alphal subunit of the receptor associated with bovine myoclonus Mol. Cell. Neurosci. 17 (2), 354-353 (2001)
Qy 509 TGTCCTGCTGATGGACCTCAAGAACTTCCCCATGGACATCCAGACGTGCACGATGCAGC 568	ntia; Peo .B., Deni
Qy 449 AGTTACTGCGCATCTTCAAGAATGGGAATGTGCTGTACAGCATCAGGCTGACCCTCATTT 508	S
QY 389 CAGACCTCTTCTTTGCTAATGAGAAAGGGGCCAACTTCCATGAGGTGACCACGGACAACA 448	ITION Bos taurus glycine receptor alpha 1 subunit (Glra1) cds, alternatively spliced. SION AF268375.1 GI:10180958
QY 329 GAGAATATCCTGATGACTCTCTGGACCTCGATCCCTCCATGCTGGACTCTATCTGGAAGC 388	RESULT 14 AF268375 AF268375 AF268375 AF268375 AF268375 AF268375 AF268375
Qy 269 TGGACTACCGGGTGAATGTCTTCCTTGCGGCAACAGTGGAATGACCCACGCCTGTCCTACC 328	Qy 1383 GCTATGGTCAGAAGATATCCACCAG 1407
OY 209 CCGTGAACGTGACCTGCAACATCTTCATCAACAGTTTCAGCTCCGTCACCAAGACCACAA 268	QY 1323 GGCTGTCCTTTCACTTTCCTCATCTTCAATATCTTCTACTGGGTTGTCTATAAAGT 1382
Qy 149 AACTTATGGGGCGAACATCTGGATATGATGCCAGGATTCGGCCCAATTTTAAAGGCCCAC 208	OY 1263 AGGAGAAACCACGCGGAAAACTCTACGTGGACTGAGCCAAGAGAATTGACACCATCTCCCG 1322

Query Match Best Local	BASE COUNT ORIGIN					cos		FEATURES Source	JOURNAL MEDLINE PUBMED REMARK	TITLE	REFERENCE	SOURCE ORGANISM	ACCESSION VERSION KEYWORDS	S73718 LOCUS DEFINITION	RESULT 15	Db	Qy		Qy E		Qу
atch 39.4%; Score 645.4; DB 10; Length 1431; cal Similarity 71.9%; Pred. No. 2.3e-168;	355 a	TLTLACPMDLKNFPMDVQTCIMQLESFGYTMNDLIFEWQEQGAVQVADGLTLPQFILK EEKDLRYCTKHYNTGKFTCIEARFHLERQMGYYLIQMYIPSLLIVILSWISFWINMDA APARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIMMAVCLLFVFSALLEYAAVNF VSRQHKELLRFRKKRHHKSPMLNLFQDDEGGEGRFNFSAYGMGPACLQAKDGISVKG ANNNTTMPPPAPSKSPEEMRKLFIORAKKIDKISFAFAHAFLIFMMFYWITYKTUP	/db_xref="G1:9247216" /translation="MYSFWILEFYLWETIVEFSLAASKEAEAARSAPKPMSPSDELDK /translation="MYSFWILEFYLWETIVEFSLAASKEAEAARSAPKPMSPSDELDK LMGRTSGYDARIRPNFKGPVIVSCNIFINSFGSIAETTMDYRVNIFLRQQWNDPRLA YNEYPDDSLDLDPSMLDSIMKPDLFFANEKCAHFHEITTDNKLLRISRNGNVLYSIRI	<pre>/codon_start=1 /product="inhibitory glycine receptor alpha 1 subunit long form" /protein id="AAB32158.2"</pre>	<pre>/gene="clral" /note="alternatively spliced; This sequence comes from /note="alternatively spliced; This sequence comes from fig. 2a and 2b; conceptual translation differs from that in published reference; GLRA1 protein; GlyR alpha 1"</pre>		/orc /db_ /tis /not		Nat. Ger 95004579 7920629 GenBank	Shlang,R., Wasmuth,J.J., Camper,S.A., Schofield,P. and O'Connell,P. A missense mutation in the gene encoding the alpha 1 subunit of the inhibitory glycine receptor in the spasmodic mouse	1 (bases 1 to 1431) Ryan, S.G., Buckwalter, M.S., Lynch, J.W., Handford, C.A.	Mus sp. M Mus sp. Eukaryota; Mammalia;	573718 \$73718.1 GI:765208			1574 TCCGCAGGAGGACGTCCACAA 1595		TCGGCTTCCCCATCGTCTTCATCTTCAACATGTTCTACTGGATCATCAAAAATCG	1454 CGGAGGAGATGCGAAAACTCTTCATCCAGCGGGCCAAGAAGATCGACAAGATCTCCCGCA 1513 1325 CTGTCTTCCCTTTCACTTTCCTCATCTTCAATATCTTCTACTGGGTTGTCTATAAAAGTGC 1384	1265 GAGAAACCACGGGGAAACTCTAAGGTGGACTGAGCCAAGAGAATTGACACCATCTCCCGGG 1324	1208 CAATGGAAGGTTCTGGCATTTATAGTCCCCAACCTCCAGCCCCTCTTCTAAGGGAAG 1264
Db	Db	Q Db	Qy Db	. Ob	Фр	Db	Qy Db	0 D 5	D 5	Db Db	Qy	Qy	Db QY	Дy	Db	oy	Db .	Qy b	. Qy	Db	Matches Qy
1118 AACGCTTGGAGGAAGATATCATCCAAGAAGTCGTTTCTATTTCCGTGGCTATGGCTTGG 1177	1070 AACACAAGGAACTGCTTCGATTTAGGAGGAGGAGAGGCGACATCACAAGAGCCCCATGCTAA 1129	GTATGCTGCCATAAATTTTGTTTCTCGTC	956 CCCGGGCCTCTTTGCCTAAGGTGTCCTACGTGAAGGCAATCGACATCTGGATGGCTGTGT 1015 	896 CTGCCCGTGTGGGCCTGGGCATCACCACCGTGCTCACCATGACCACCACAGAGCTCTGGCT 955	836 CCAGCCTACTCATCGTCATCCTGTCCTGTCTGCTTCTGGATCAACATGGATGCTGCCC 895 			716 GGGATGAGGATCTAGGGTGGTTGTACCAAGGGGTGACTCTGCCCCAGGTTATCTTGC /15	TICLE CONTROL TO THE			476 ATGTGCTGTACAGCATCAGGCTGACCCTCATTTTGTCCTGCCTG	416 GGCCCACTTCCATGAGGTGACCACGGACAACAGTTACTGCGCATCTTCAAGAATGGGA 475	TCGATCCCTCCATGCTGGACTCTATCTGGAAGGCAGACCTCTTCTTTGCTAATGAGAAAG	GCAGCAGTGGAACGACCCCCGTCTGGCCTACAATGAATACCCTGATGACTCTCTGGACC			213 TCAACAGTTTCAGCTCGGTCACCAAGACCACAATGGACTACCGGGTGAATGTCTTCTTGC 295	176 ATGCCAGGATTCGGCCCAATTTTAAAGGCCCACCCGTGAACGTGACCTGCAACATCTTCA 235	155 CCAAGCCTATGTCACCCTCGGACTTCCTGGATAAGCTCATGGGGAGGACTTCTGGGTATG 214	

Search Job ti	B	Qy	DЬ	Qy	Db	Qy	DЬ	Qy
Search completed: June 30, 2003, 22:23:46 Job time : 4235 secs	1370 TCAACATGTTCTACTGGATCATCTATAAGATCGTCCGGAGAGAGA	1352 TCAATATCTTCTACTGGGTTGTCTATAAAGTGCTATGGTCAGAAGATATCCACCA 1406	1310 AGAGAGCCAAGAAGATCGACAAGATATCTCGCATCGGTTTCCCCCATGGCCTTCCTCATCT 1369	1292 ACTGAGCCAAGAGAATTGACACCATCTCCCGGGCTGTCTTCCCTTTCACTTTCCCTCATCT 1351	1250 CCACTAACCCGCCTCCTGCGCCATCCAAGTCCCCGGAGGAGATGCGGAAACTCTTCATCC 1309	1235 CCCAACCTCCCAGCCCCTCTTCTAAGGGAAGGGAAACCCACGCGGGAAACTCTACGTGG 1291	1190 GCCCAGCCTGTCTGCAGGCCAAGGATGGCATCTCTGTCAAGGGTGCCAACAACAACAACAACA 1249	1178 GCCACTGCCTGCAGGCAAGAGATGGAGGTCCAATGGAAGGTTCTGGCATTTATAGTC 1234

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-DB--GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINNATCH+0.1 -LOOPCL=0 -LOOPEXT=0
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-DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

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Baughn,M.R., Yang,J., Yao,M.G., Lal,P., Walla,N.K., Gandhi,A.R.,
Hafalla,A.J., Nguyen,D.B., Patterson,C., Elliott,V.S.,
Tribouley,C.M., Lu,D.A., Xu,Y., Reddy,R., Hernandez,R.,
Borowsky,M.L., Lo,T.P., Lu,Y., Policky,J.L., Greene,B.D.,
Sanjanwalla,M.S., Raumann,B.E., Burfordd,N., Ison,C.H., Lee,E.A.,
Ding,L., Das,D., Kallick,D.A., Khan,F.A. and Seilhamer,J.J.
Patent: WO 0212340-A 52 14-FEB-2002;
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       LeuTyrSerIleArgLeuThrLeuIleLeuSerCysLeuMetAspLeuLysAsnPhePro
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                                            WO 0058461-A 1 05-OCT-2000, HOERBRAND GUDRUN (DE)
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SDFLDKLMGRTSGYDARIRPNFKGPPVNVTCNIFINSFSSITKTMDYRVNVFLRQQW
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EYAAINFYSRQHKEFIRLRRQRRQRLEDDIIQESRFYFRGYGLGHCLQARDGGPMEG
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                                                                                                                                     Unpublished 2 (bases 1
                                                                                                                                                      Localization of spinal cord
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Groemer, T.-W., Becke
                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                          Mus musculus
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                  /tissue_type="spinal cord"
1. .1251
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/note="mmGlra4"
                                                       /organism="Mus
/strain="B6C3/E
                                   /chromosome="X"
                                               /db_xref="taxon:10090"
                                                                                                                                                                          Becker, C.-M. and Becker, K.
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Murinae; Mus
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                                LysPheHisLeuGluArgGlnMetGlyTyrTyrLeuIleGlnMetTyrIleProSerLeu
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IDIWMAVCLLFVFAALLEYAAVNFVSROHKEFMFLRRORRQMEEDIIRESRFYFRG
YGLGHCLQARDGGPMEGSSIYSPQPPTPLLKEGETMRKLYVDRAKRIDTISRAVFPFT
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/note="ligand-gated ion channel"
/codon_start=1
/product="glycine receptor alpha
/protein_id="AAL69899.1"
/db_xref="GI:18448711"
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1 (bases 1 to 2045)

1 (bases 1 de Saint Jan, D., Leulier, F., Droccetter, de Saint Jan, D., Leulier, D., Droccetter, de Saint Jan, 
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                                                                                                                             /organism="Danio rerio"
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/tissue_type="brain"
/dev_stage="adult"
                                                                                                                                                                                                    25 rue du Dr Roux,
Location/Qualifiers
                 /gene="glyR alpha"
/codon_start=1
    /product="glycine receptor
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TACACCATGAACGATCTGATCTTCGAGTGGCTTTCTGATAACCCT---GTGCAGGTTGCG
                                                                       TyrThrMetLysAspLeuValPheGluTrpLeuGluAspAlaProAlaValGlnValAla
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INMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLIVFAALLEY
AAVNIYSRQHKEFIRLKKQRRQRIEEDLVRESRGFYFRGYGLGHCLQTKDGTAVEGS
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DPRLAYSEYPDASLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFQNGNVL
YSIRLTLILSCPMDLKNFPMDJQTCTMQLESFGYTMNDLIFEMJSDNPYQVADDLTLP
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/db_xref="GI:11322384"
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2155780
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1 (bases 1 to 1857)

Grenningloh,G., Schmieden,V., Schofield,P.R., Seeburg,P.H., Siddique,T., Mohandas,T.K., Becker,C.M. and Betz,H. 

Alpha subunit variants of the human glycine receptor: primary structures, functional expression and chromosomal localization of
                                                                                                                                                                                 EMBO J. 9 (3), 771-776 (1990)
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glycine receptor; inhibitory glycine receptor;
                   X52008.1 GI:31848
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                                                                  bp mRNA linear PRI 28-MAY-199
binding subunit of inhibitory glycine
 strychnine binding.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="brain"
/dev_stage="fetal" Location/Qualifiers 1. .1857

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/gene="GLYRA1" 388. .1746

/gene="GLYRA1"

/note="strychnine binding alpha-2 subuni

Page 6

BASE

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Query Match: DB:

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Score:

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US-10-075-846-4 (1-431) x HSGLYRA1
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AspLeuGlyCysCysThrLysHisTyrAsnThrGlyLysPheThrCysIleGluValLys
                                                                                                                                                                                                       GTCCAGACCTGTACAATGCAGCTGGAG------
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                                                                        ProAlaValGlnValAlaGluGlyLeuThrLeuProGlnPheIleLeuArgAspGluLys 242
                                                                                                                                                  LeuSerLeuSerValGlyTyrThrMetLysAspLeuValPheGluTrpLeuGluAspAla
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PQFILKEEKELGYCTKHYNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSWVSF
WINMDAAPARVALGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLFVFAALLE
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SDFLDKLMGRTSGYDARIRPNFKGPPVNVTCNIFINSFGSVTETTMDYRVNIFLRQQW
NDSRLAYSEYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHDVTTDNKLLRISKNGKV
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/protein_id="CAA36257.1"
/db_xref="GI:31849"
/db_xref="SWISS-PROT:P23416"
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                                                                                                                             AGTTTTGGGTACACGATGAATGACCTGATATTTGAGTGGTTAAGTGATGGT 1011
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Submitted (30-MAR-2001) Groot-Kormelink P.J., Department of Submitted (30-MAR-2001) Groot-Kormelink P.J., Department of Submitted (30-MAR-2001) Groot-Kormelink P.J., Department of Submitted (30-MAR-2001) Brunswick Square, London, WClN lax, UNITED KINGDOM
                                                                                                                                                                                                                                                                                                                                                l (bases 1 to 1359)
Beato, M., Groot-Kormelink, P.J., Colquhoun, D. and Sivilotti, L.G.
Concentration dependence of single channel currents through rat
recombinant alpha 1 glycine receptors
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Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                               Unpublished
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                                                       /tissue_type="whole brain"
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1. 1359
                                                                                                                           /strain="Sprague-Dawley males"
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                                      /function="ion channel
                                                                                                                                                                 organism="Rattus norvegicus"
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Rodentia;
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NDSRLAYSEYPDDSLDLDPSMLDSIWKPDLFFAAEKGANFHDVTDNKLLRISKNGKV
LYSIRLTLTLSCPMDLKNFPMDVQTCTMOLESFGYTMNDLIFEMLSDGYVQNAEGLTL
PQFILKEEKELGYCTKHYNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSWVSF
WINMDAAPARVALGITTVLTMTTQSGGSRASLPKVSYVKAIDIMMAVCLLFVFAALLE
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/protein_id="CAC35981.1"
/db_xref="GI:13548661"
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4 Rattus norvegicus
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1 (kases 1 to 3160)
Kuhse, J., Kuryatov, A., Maulet, Y., M
Betz, H. Kuryatov, A., Maulet, Y., M
Alternative splicing generates two
Alternative splicing generates two
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                                                                                                                                                                           inhibitory glycine receptor ett. 283 (1), 73-77 (1991)
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/protein_id="caA3471.1"
/db_xref="GI:288345"
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NDSRLAYSEYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHDVTTDNKLLRISKNGKV
                                                                                                       /organism="Rattus norvegicus
/db_xref="taxon:10116"
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PQFILKBEKELGYCTKHYNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSWVSF
WINMDAAPARVALGITTVLTMTTQSSGSRASLFVAYSYKYLIDIMMAVCLLFVERALLE
YAAVNEVSRQHKEELLGKRRQKRQNKEEDVTRESRFNESGYGMGHCLQVKDGTAVKAT
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Submitted (28-JAN-1991) F. Hishinuma, Mi
Life Sciences, 11 Minamiooya, Machida-sh
2 (bases 1 to 3865)
Akagi, H., Hirai, K. and Hishinuma, F.
Cloning of a glycine receptor subtype ex
spinal cord during a specific period of
FEBS Lett. 281 (1-2), 160-166 (1991)
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                                                    /strain="Wistar"
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ya, Machida-shi, Tokyo 194, Japan
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WINMDAAPARVALGITTVLTMTTGSGSGSASLEKVSYVKAIDLWMAVCLLFVERALLE
VAAVNFYSROHKEFLKLRROKRONKEEDVTRESFYNFSGYGMGHCLQVKDGTAVKAT
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U93917
U93917.1 GI:3
                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3069)
Mikolic,Z., Laube,B., Weber,R.G., Lichter,P., Kioschis,P.,
Poustka,A., Mulhardt,C. and Becker,C.M.
The human glycine receptor subunit alpha3. Glra3 gene structure,
chromosomal localization, and functional characterization of
alternative transcripts
J. Biol. Chem. 273 (31), 19708-19714 (1998)
                                                    Direct Submission
Submitted (17-MAR-1997) Biochemistry, University
Erlangen-Nuremberg, Fahrstr. 17, Erlangen 91054,
                                                                                                                         98344067
9677400
                                                                                               Nikolic,
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                                                                                                           (bases 1 to 3069)
                           Location/Qualifiers
1. .3069
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receptor alpha
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LysAspLeuGlyCysCysThrLysHisTyrAsnThrGlyLysPheThrCysIleGluVal
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                                                  SerLeuSerLeuSerValGlyTyrThrMetLysAspLeuValPheGluTrpLeuGluAsp
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INMDAAPARVALGITTYVLTMTTQSSGSRASLPKYSYVRALDIWAAVCLLFVFSALLEY
AAVNEVSROHKELLRERKKNKNDDEVRESRFSFTAYGMGPCLQAKDGMIPKGPNHPV
AAVNEVSROHKELLRERKKNKNDDEVRESRFSFTAYGMGPCLQAKDGMIPKGPNHPV
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547 c 583 g 977 t
                                      GTACAAGTGGCAGAAGGACTCACTTTGCCCCAGTTTCTGTTGAAAGAAGAA
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AJ310838.1 GI:13548662
glycine receptor alpha 3
Norway rat.
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                                                                                                                                                  Direct Submission
Submitted (30-MAR-2001) Groot-Kormelink P.J., Departmen Pharmacology, The School of Pharmacy, 29/39, Brunswick London, WClN 1AX, UNITED KINGDOM
                                                                                                                                                                                                                                                               1 (bases 1 to 1443)
Beato, M., Groot-Kormelink, P.J., Colquhoun, D. and Sivilotti, L.G.
Concentration dependence of single channel currents through rat
                                                                                                                                                                                                                                                                                                                               Rattus norvegicus
Eukaryota; Metazoa;
                                                                                                                                                                                                            Groot-Kormelink,
                                                                                                                                                                                                                          Unpublished 2 (bases 1
                                                                                                                                                                                                                                                   recombinant alpha
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                                                                                                                                                                                                                                                                                                                                                                                                              norvegicus mRNA for
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                                      /dev_stage="8-12
1. .1443
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Rodentia;
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RESRFSFTAYGMGPCLQAKDGVVPKGPHAQQD"
RESRFSFTAYGMGPCLQAKDGVVPKGPHAQQD"
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Kuhse, J., Schmieden, V. and Betz, H.

Identification and functional expression of subunit of the inhibitory glycine receptor J. Biol. Chem. 265 (36), 22317-22320 (1990) 91093073

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                                                                                                                                                                                                                                                                                                                              RATIGRAS
RATIGRAS
RAT inhibitory glycine receptor alpha sub
M55250 M38385
M55250.1 GI:204882
inhibitory glycine receptor.
Rat (strain Wistar) adult brain, cDNA to
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                 Rattus norvegicus
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                          Rattus
                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria;
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-----ATGCCAAAGAGCGCCGATGAAATGAGGAAGGTCTTCATCGAC
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1. . 2413
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  /product="inhibitory
                           /gene="inhibitory
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                                                                                                                                                   /organism="Rattus norvegicus"
                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                       Rodentia;
                           glycine
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Sciurognathi; Muridae; Murinae;
  glycine receptor
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                              TyrThrMetLysAspLeuValPheGluTrpLeuGluAspAlaProAlaValGlnValAla
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                   TACACGATGAATGATCTCATTTTCGAATGGCAAGATGAAGCACCA---GTACAAGTGGCT
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                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1715)
Grenningloh,G., Schmieden,V., Schofield,P.R., Seeburg,P.H., Siddique,T., Mohandas,T.K., Becker,C.M. and Betz,H.

Alpha subunit variants of the human glycine receptor: primary structures, functional expression and chromosomal localization
                                                                                                                                                                                                                                                                                                                                                                       HSGLYRA2
H.sapiens alpha-1
                                                                                                                                                                                                                                                                                                glycine receptor;
Homo sapiens.
                                                                                                                                                  EMBO J. 9 (3), 771-776
                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                          Location/Qualifiers
1. .1715
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| strychnine |
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binding sul
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RNA linear PRI 28 subunit of inhibitory

28-MAY-1993

1668 431

1455

376

1395 348 1335

368

328

1275 308 1215 1155

288

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248

glycine

receptor;

strychnine binding

Euteleostomi;

of.

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                                                    CysSerProLeuProSerLeuSerLeuSerValGlyTyrThrMetLysAspLeuValPhe
                                                                                                           LysAsnPheProMetAspIleGlnThrCysThrMetGlnLeuGluSerSerSerIleLeu
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24 a 480 c 407 g 404 t
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297. .1646
/gene="GLYRA2"
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70.18%
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Bos taurus glycine r
cds, alternatively s
AF268375
AF268375.1 GI:10180
                                            Direct Submission
Submitted (17-MAY-2000) Neurobiology Program, Garvan Institute
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Mammalia; E
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11178872
                                                                                                                                                       A nonsense mutation in the alphal subunit of receptor associated with bovine myoclonus MOI. Cell. Neurosci. 17 (2), 354-363 (2001)
                                                                                            Healy, P.J. and Schofield
                                                                                                        Pierce, K.D.,
                                                                                                                                                                                                 Pierce, K.D., Handford, C.A., M. Healy, P.J. and Schofield, P.R.
                                                                                                                                                                                                                                          Bovidae; Bovinae; Bos.
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lerce, K.D., Handford, C.
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                                                                                                                                                                                                                                                                                  taurus
                                                                                                                                                                                                                                                                                                taurus
 /organism="Bos taurus"
/db_xref="taxon:9913"
                                       Location/Qualifiers
                                                                                                                                                                                                                                                      ; Metazoa; Chordata; Craniata; Vertebrata; Eute
Eutheria; Cetartiodactyla; Ruminantia; Pecora;
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/note="Glralins;
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Submitted (71-MAR-2001) Biochemistry,
Submitted (71-MAR-2001) Biochemistry,
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AF362764
                                                                                                                                                         Mus musculus
Eukaryota; Metazoa; Chordata; Cran
Eukaryota; Betheria; Rodentia; Sciu
1 (bases 1 to 1392)
Noegel,S., Becker,C. and Becker,K.
Different glycine receptor isoform
                                                                                                       2 (bases 1 to 1392)
Noegel, S., Becker, C.
                                                                                                                                 Unpublished
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/db_xref="taxon:10090"
                          /organism="Mus musculus
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                           sThrMetGlnLeuGluSerSerSerIleLeuCysSerProLeuProSerLeuSerLeuSe
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                                                                               Danio rerio
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 1628)
                                                                                                                                                                                 Danio rerio mRNA for glycine
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alphaz1 subunit; glyci
2 (bases 1 to 1)
David-Watine, B.,
                                    Direct Submission
Submitted (27-APR-1998)
U261 - Institut Pasteur,
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Roux, 75724 Paris
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TITLE A novel alpha subunit of the glycine receptor from zebrafish: JOURNAL DEPUNDENCE AND CONTROL OF THE STATES AND CONT
A novel alpha subunit of the glycine receptor from zebrafish. Dipublished Location/Qualifiers 1. 1628 1. 1627 1. 1628 1. 16

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Oy 418 uLeuArgGluGlyGluThrThrArgLysLeuTyrVal 430	Qy 399 ArgAspGlyGlyProMetGluGlySerGly-IleTyrSerProGlnProProAlaProLe ::: ::::: ::: Db 1209 AAAGACGGCATGGCAATCAAGGGCAACAACAACAACGGGCCCACCTCCACCCAC	Qy 380 IleGlnGluSerArgPheTyrPheArgGlyTyrGlyLeuGlyHisCysLeuGlnAla ::	Qy 360 HisLysGluPheIleArgLeuArgArgGlnArgArgGlnArgLeuGluGluAspIle	Qy 340 LeuLeuPheValPheAlaAlaLeuLeuGluTyrAlaAlaIleAsnPheValSerArgGln	Qy 320 ArgalaSerLeuProLysValSerTyrValLysAlaIleAspIleTrpMetalaValCys	Qy 300 AlaArgValGlyLeuGlyIleThrThrValLeuThrMctThrThrGlnSerSerGlySer	Qy 280 SerLeuLeulleValIleLeuSerTrpValSerPheTrpIleAsnMetAspAlaAlaPro	Qy 260 GluValLysPheHisLeuGluArgGlnMetGlyTyrTyrLeuIleGlnMetTyrIlePro	Qy . 240 AspGluLysAspLeuGlyCysCysThrLysHisTyrAsnThrGlyLysPheThrCysIle :::	Qy 220 GluAspAlaProAlaValGlnValAlaGluGlyLeuThrLeuProGlnPheIleLeuArg	Qy 200 LeuProSerLeuSerLeuSerValGlyTyrThrMetLysAspLeuValPheGluTrp	Qy 180 ProMetAspileGlnThrCysThrMetGlnLeuGluSerSerSerIleLeuCysSerPro	Db 540 GTTTTATACAGTATAAGAATAACACTGGTTCTGGCCCTGCCCCATGGACCTGAAGAATTTC
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SUMMARIES

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44	۱ د) i	<u>ی</u> ا	24	24	22	22	15	14	23	20) <u>-</u>	, ,	10	21	22	22	21	21	23	19	19	20	22	22	21	20	24	23	17	20	24	24	24	22	22	24	22	24	24	22	21	24	13	21	24	DB
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ALIGNMENTS

RESULT 1 AAD33667 K K K K K K K X E X T X A C X 01-JUL-2002 (first entry) AAD33667 standard; cDNA; 1874 BP Human TRICH-22 cDNA.

Human; transporter and ion channel; TRICH-22; transport disorder; angina; amyotrophic lateral sclerosis; cystic fibrosis; neuromuscular disorder; cardiac disorder; polymyositis; diabetes; neurological disorder; cancer; depression; schizophrenia; anaemia; Wilson's disease; Cushing's disease; cell proliferated disorder; infertility; arteriosclerosis; gene therapy; alzheimer's disease; Parkinson's disease; Huntington's disease; allergy; and the control of acquired immune deficiency syndrome; myasthenia gravis; multiple sclerosis; immunological disorder; metabolic scleroderma

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mycarditis, prostate cancer, cardiac disorders associated with

ctransport e.g. polymyositis, bradyarrythmia, dermatomyositis, angina,

cneurological disorders associated with transport e.g. amnesia, bipolar

cdisorder, depression, Tourette's disorder, schizophrenia, other disorders

cassociated with transport e.g. neurofibromatosis, sickle cell anaemia,

cwilson's disease, cataracts, infertility, hyperglycaemia, hypoglycaemia,

cyoitre, Cushing's disease, hypercholesterolaemia and cystinuria. Cell

cyoitre, Cushing's disease, hypercholesterolaemia and cystinuria. Cell

cyoitre, Cushing's disease, hypercholesterolaemia and cystinuria.

cell

cyoitre, Cushing's disease, hypercholesterolaemia and psoriasis.

carteriosclerosis, atherosclerosis, bursitis, hepatitis and psoriasis.

cushem and other certorosis, dementia and other extrapyramidal disorder,

conversellar, disorder, prion disease, metabolic disease of the nervous

system and other developmental disorders of the central nervous system,
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reene BD, Sa,
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25-AUG-2000;
31-AUG-2000;
                                                                                                                                                                                                                                                                                                   designated TRICH and nucleic acid molecules encoding such polypeptides. TRICH sequences are useful for diagnosis, treatment and prevention of transport, muscle, neurological, immunological and cell proliferative disorders. Transport disorders include akinesia, amyotrophic lateral sclerosis, ataxia telangiectasia, cystic fibrosis, Becker's muscular dystrophy, diabetes mellitus, diabetes insipidus, myasthenia gravis, myocarditis, prostate cancer cardiac disorders.
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epilepsy; mental d
muscle disorder; s
                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to human transporter and ion channel polypeptides designated TRICH and nucleic acid molecules encoding such polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human transporters and ion channels polypeptides and polynucleotides for diagnosing, preventing or treating t neurological, muscle, immunological and cell proliferati
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                              neuromuscular disorders, metabolic, endocrine and toxic myopathies,
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               paralysis, mental disorders including mood,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disorder; autoimmune thyroiditis; rheumatoid arthritis;
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; 2000US-226410P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
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GluLysAspLeuGlyCysCysThrLysHisTyrAsnThrGlyLysPheThrCysIleGlu
                                                                                     ProSerLeuSerLeuSerValGlyTyrThrMetLysAspLeuValPheGluTrpLeuGlu
------AGGTTTGGCTACACCATGAAAGACCTCGTGTTTGAGTGGCTGGAA
                                                                                                                                                                                                                                                                  AACTTCCATGAGGTGACCACGGACAACAAGTTACTGCGCATCTTCAAGAATGGGAATGTG
                                                                                                                                                                                                                                                                                AsnPheHisGluValThrThrAspAsnLysLeuLeuArgIlePheLysAsnGlyAsnVal
                                                                                                                                                 ATGGACATCCAGACCTGCACGATGCAGCTTGAG------
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                                        Prepn. of N-terminal extracellular site protein E.coli transformed by a plasmid comprising the t
  The sequence beta-subunit.
                     Claim 1; Page 2; 12pp; Japanese.
                                    binding
                                                                  WPI;
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                                                                                             05-OCT-1990;
                                                                                                          05-OCT-1990;
                                                                                                                        19-MAY-1992
                                                                                                                                      JP04144683-A
                                                                                                                                                                   Expression
                                                                                                                                                                               GABA-A receptor beta-subunit.
                                                                                                                                                                                               08-DEC-1992
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given is the gamma-aminobutyric acid (GABA) A receptor This sequence is used in an expression plasmid operably
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linked to the tac promoter, a ribosome binding sequence, the E. coli outer membrane protein OmpF signal peptide coding sequence and a sequence coding for the N-terminal extracellular site of either the gamma-aminobutyric acid (GABA) A receptor alpha-subunit or the glycine receptor alpha-subunit. This expression plasmid can be used to transform E. coli to produce an N-terminal extracellular site-protein of ion channel direct binding type receptor.
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GluValLysPheHisLeuGluArgGln
                                   GAAGAGAAGGATCTGAGATACTGCACCAAGCACTACAACACAGGTAAATTCACCTGCATT
                                                                                                                                                                                 GACCCATCCATGTTGGATTCCATCTGGAAGCCTGACTTGTTCTTTGCCAATGAGAAGGGG
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                                                                                                                                              LeuProSerLeuSerLeuSerValGlyTyrThrMetLysAspLeuValPheGluTrpLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (1) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (1). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vesospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB19912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. AB19913 and AB19914
                                                                                                                                                                                                                                                                                                                                                                              Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
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<pre>p protection; insecticide; nematocide; ss. us sanguineus. Location/Qualifiers 6172170 /*tag= a /product= "R. sanguineus GluCll p: /note= "This region is specifical"</pre>	SULT 6 D21397 AAD21397 standard; cDNA; AAD21397; AAD21397; 28-JAN-2002 (first entr) R. sanguineus glutamate-o		Db 35654 ACCCCAGACCTTACTCCTCACCTGTTCTCTCCTGCCTGTTCTGATCCTACCCCTACCCCC 35713 Oy 193SerSerIleLeuCysSerProLeuProSerLeuSerLeuSerValGlyTyrThrM 211 :::	192 35534 AGGAGAGGAGTCTGTAATCTTCCTGATTTACCTGCCCACTCAGGATGGGCCCATGAGACA 192 35594 ACTGACCAAGTGTCCTCTCCAGAAAAGTTTTCCTTTCCATAATGAGCATGAAGCTCCTAA 192	Db 35354 GCTCTGAGGCTAGCTCAGCTTAAGACATGTTCTCTGGGTACACATGCTTACTCCCCTCGGCT 35413 Oy 192	Db 35174 GGCATGAGCCCTCATGAACTTGTGTGTGAATAACTTGACATGTTCAGACATTAG 35233 Qy 192

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--glutamate-gated chloride channel proteins (GluCl1 and GluCl2)
and nucleic acid molecules encoding such proteins. GluCl channel
proteins are useful for identifying modulators. The compounds
identified as modulators are useful for insecticidal, mitacidal
and/or nematocidal treatment for use in animal and human health
and/or crop protection. The compounds are also useful in screening
for and selecting compounds active against parasitic invertebrate
species relevant to animal and human health, including worms,
fleas, ticks, mites and lice. Heterologous cell lines expressing
functional GluCl1 and GluCl2 channel functional forms are useful
for establishing functional or binding assays to identify novel
GluCl1 channel modulators. The present sequence is R. sanguineus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel L-glutamate-gated chloride channel proteins from Rhipicephalus sanguineus for identifying compounds which modulate the channel proteins, which are useful as insecticides, anthelmintics and
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                                                                                                                                                                                                                                                                                                                                                             The invention relates to nucleic acid encoding lepidopteran glutamate-gated chloride channels are a family of ligand-gated chloride channels unique to invertebrates. The DNA of the invention is used for recombinant production of lepidopteran glutamate-gated chloride channel and this is used, optionally in the form of membrane preparations or recombinant cells, in specific-binding or functional assays for identifying potential insecticides. The present sequence is HEGEZ clone CDNA encoding full insections.
                                                                                                                                                                                                                                                                                                             Sequence 4621
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                                     GAATGCATGAACGGTGGGAAGATCAACTTTCGAGAGAAGGAGAAGCAGATCCTGGATCAG
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/note= "This translational exception occurs while
decoding for the alternative version (AAE16439)"
/transl_except= (pos:177..188, aa:LVLL)
/note= "Insertion of 6 bases alters the reading fr
/transl_except= (pos:762..764, aa:K)
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chloride channel"
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(pos:1125..1127, aa:R)
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(pos:981..983, aa:L)
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                 GluGlySerGlyIleTyrSerProGlnProProAla
                                                     CACAGATAGCAACACCACCTTTGCTATGAAACCCTTGGTGCGCGGCGGCGTGGTATC
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Note: This sequence SEQ.ID.NO.11 is stated to be similar to the sequence shown in sequence listing of the specification. However these sequences differ.
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HEG3E(4)-2 plasmid; cyclic; circular; ds.
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                                                                                                                                                                                                                                              ThrThrValLeuThrMetThrThrGlnSerSerGlySerArgAlaSerLeuProLysVal
                                                                                                                                                                                                                                                                                                                               CysThrLysHisTyrAsnThrGlyLysPheThrCysIleGluValLysPheHisLeuGlu
                                                                                                                                                                                                                                                                                                                                                                                                                              GTGAAAAACTTACACCTGCCTCGGTTCACGCTG
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                                                                                                ArgLeuArgArgArgGln 370 :::
                                                                                                                                   CTACTAGAGTTTGCGCTCGTCAACTATGCGTCTCGCTCTGACATGCACCGAGAGAACATG
                                                                                                                                                                                    TCCTACACGAAAGCCATTGATGTCTGGACTGGGTTATGTCTCACATTCGTATTCGGAGCG
                                                                                                                                                                                                SerTyrValLysAlaIleAspIleTrpMetAlaValCysLeuLeuPheValPheAlaAla
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                                    standard;
                                                                                     AAGAAAGCGAGACGGGAG
                                                                                                                                                            LeuLeuGluTyrAlaAlaIleAsnPheValSerArg-----GlnHisLysGluPheIle
                                                                                                                                                                                                                                    ACGACTTTACTTACAATGGCGACCCAGTCGTCAGGCATCAACGCGTCCCTACCACCGGTG
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                                                                                                                                                                                                      DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a purified nucleic acid molecule encoding CC Dermancentor variabilis (DV) (American dog tick) ligand gated ion CC channel/L-glutamate gated chloride channel (IGIC/GluCl) protein.
CC LGIC/GluCl DNA is useful for identifying a compound that modulates CC glutamate-gated channel protein activity and for identifying a modulator Of LGIC/GluCl DNA is used for establishing CC insecticidal activity for use in treating parasitic infections in humans CC insecticidal activity for use in treating parasitic infections in humans CC or animals, as hybridisation probes to isolate related genes from other CC organisms to establish additional pesticide drug screens and also used CI ncompetition binding experiments or for functional chloride channel CC assays to screen for compounds that activate, block or modulate the CC channel. Heterologous expression of LGIC/GluCl protein allows the CC pharmacological analysis of compounds active against parasitic CC invertebrate species relevant to animal and human health, especially in the treatment of tick infestations directly related to Dv. LGIC/GluCl CC modulators act as effective insecticidal, acaricidal, mitacidal and/or crop compounds active against parasitic compounds act as effective insecticidal, acaricidal, mitacidal and/or crop compounds carried to the treatment of the modulators are useful for treatment or diagnosis of compounds carried to the treatment or diagnosis of compounds carried to the treatment or crop compounds carried to the treatment or diagnosis of compounds carried to the treatment or diagnosis of compounds carried to the channels.
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                                                                                      LeuAspLysLeuMetGlyArgThrSerGlyTyrAspAlaArgIleArgPro------
---AsnPheLysGlyProProValAsnValThrCysAsnIlePheIleAsnSerPheSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders. The present sequence is Rhipicephalus
                                                                 TTGGACAGCATCATTGGCCAG----GGTCGTTATGACTGCAGGATCCGGCCCATGGGAATT
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Key
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ATCAGAATATCCTTGGTGCTTTCATGTCCGATGAACCTGAAATTTTATCCTTTGGATAAA 420
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Location/Qualifiers
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                                                                                   GluCl1;
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                             The invention relates to Rhipicephalus sanguineus (brown dog tick)
L'glutamate-gated chloride channel proteins (GluCil and GluCi)
and nucleic acid molecules encoding such proteins. GluCil channel
proteins are useful for identifying modulators. The compounds
identified as modulators are useful for insecticidal, mitacidal
and/or nematocidal treatment for use in animal and human health
and/or crop protection. The compounds are also useful in screening
for and selecting compounds active against parasitic invertebrate
species relevant to animal and human health, including worms,
fleas, ticks, mites and lice. Heterologous cell lines expressing
functional GluCil and GluCil channel functional forms are useful
for establishing functional or binding assays to identify novel
GluCil channel modulators. The present sequence is R. sanguineus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel L-glutamate-gated chloride channel proteins from Rhipicephalus sanguineus for identifying compounds which modulate the channel proteins, which are useful as insecticides, anthelmintics and
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                                                                                                                                                                                                                                                                                                                                                Sequence 2138
                                                                                                                                                                                                                                                                                                                                                                      GluCl1 cDNA clone, T12.
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             LeuAspSerIleTrpLysProAspLeuPhePheAlaAsnGluLysGlyAlaAsnPheHis 143
                                                                                                      SerValThrLysThrThrMetAspTyrArgValAsnValPheLeuArgGlnGlnTrpAsn ::: ||||||||
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 CCGGACAAGCTTTGGAAGCCGGACCTGTTTTTCTCCAACGAGAAAGAGGGGACACTTCCAC 747
                                                               AspProArgLeuSerTyrArgGluTyrProAspAspSerLeuAspLeuAspProSerMet
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                                              GACGAGAGACTCCAGTACGACGACTTGGGCGGCCAGGTTCGCTACCTGACGCTCACCGAA
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region is specifically referred in claim
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clone T82; ss
                                                                                         Brown dog tick; glutamate-gated chloride channel; GluCl2; crop protection; insecticide; nematocide;
                                                                                                                           R. sanguineus
                                                         Rhipicephalus
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                                                                                                                                                                                                                                                                                      CGGCAGAACATGCAGAAGCAGAAGCAGAGGAAATGGGAGCTCGAGCCGCCCCTGGACTCG
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                                                                                                                                                (first entry)
                                                                                                                         glutamate-gated chloride channel 1 cDNA clone,
                                                        sanguineus
                      Location/Qualifiers 502..1854
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"R. sanguineus GluCl1 protein,
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C L-glutamate-gated chloride channel proteins (GluCl and GluCl2)
C and nucleic acid molecules encoding such proteins. GluCl channel
C proteins are useful for identifying modulators. The compounds
C identified as modulators are useful for insecticidal, mitacidal
C and/or nematocidal treatment for use in animal and human health
C and/or crop protection. The compounds are also useful in screening
C for and selecting compounds active against parasitic invertebrate
C species relevant to animal and human health, including worms,
C fleas, ticks, mites and lice. Heterologous cell lines expressing
C functional GluCl1 and GluCl2 channel functional forms are useful
C for establishing functional or binding assays to identify novel
C GluCl channel modulators. The present sequence is R. sanguineus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                      GACGAGAGACTCCAGTACGACGACTTGGGCGGCCAGGTTCGCTACCTGACGCTCACCGAA
                                                                                                                                                         AspProArgLeuSerTyrArgGluTyrProAspAspSerLeuAspLeuAspProSerMet 123
                                                                                                                                                                                           AGAATTGATGACGTCACCATGGAGTACACAGTGCAAATGACGTTCAGAGAGCAGTGGCGG
                                                                                                                                                                                                                         SerValThrLysThrThrMetAspTyrArgValAsnValPheLeuArgGlnGlnTrpAsn
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                                                                                                                                                                                       Gamma-aminobutyric acid; GABA; tick infestation; mite; antiparasitic; GABA-gated chloride channel; recombinant expression; domestic animal;
                                                                                                                                                                                                                                                                                                                                                    AAD22072 standard; DNA; 1614
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                                                                                                                                                                                                                                                                                                                                                                                                                        GACCACCTGGAGGACGGCGCCACCACGTTCGCCATGAGGCCGCTGGTGCAC
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                                                                  "GABA-gated chloride channel protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to gamma-aminobutyric acid (GABA)-gated chloride channels and their corresponding nucleic acid molecules. GABA-gated chloride channel proteins and DNA's are useful for preventing and treating tick infestation, particularly in humans, dogs, cattle, horses, deer, or other wild or domesticated animals. The nucleic acids are useful as hybridisation probes or Polymerase Chain Reaction primers for identifying the presence of Dermacentor variabilis GABA-gated chloride channel nucleic acid or DNA's encoding for a GABA receptor. The nucleic acids are also useful for the recombinant expression of D. variabilis GABA-gated chloride channel proteins exert toxic effects on other ticks or related parasites such as mites. The present sequence is Dermacentor variabilis clone 5 GABA-gated chloride channel DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polypeptide useful for preventing or treating tick infestation, in humans, dogs, cattle, horses, deer, or other wild or domesticated animals, comprises the Dermacentor variabilis gamma-aminobutyric acid (GABA)-gated chloride channel -
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             MetAspLeuLysAsnPheProMetAspIleGlnThrCysThrMetGlnLeuGluSerSer 193
                                                                                                                                          CTCGAGAGCATGACTGTGGGCGCTGAAGTGGCCGAGAGGATCTGGGTACCCGACACCTTC
                                                                                                                                                         ---AspSerLeuAspLeuAspProSerMetLeuAspSerIleTrpLysProAspLeuPhe :::|||::: :::
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                                                                                                                                                                                                                                                               CysAsnIlePheIleAsnSerPheSerSerValThrLysThrThrMetAspTyrArgVal
                                                                                             TTCGCCAACGAGAAGAGCGCCTACTTTCATGCGGCCACAACGCCCAACACTTTCCTCCGC
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                                                                                                                                                                          Gamma-aminobutyric acid; GABA; tick infestation; mite;
GABA-gated chloride channel; recombinant expression; do
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                                                                                               Location/Qualifiers
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                                      "GABA-gated chloride channel protein".
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chloride channel proteins and DNA's are useful for preventing and treating tick infestation, particularly in humans, dogs, cattle, horses, deer, or other wild or domesticated animals. The nucleic acids are usefu as hybridisation probes or Polymerase Chain Reaction primers for identifying the presence of Dermacentor variabilis GABA-gated chloride channel nucleic acid or DNA's encoding for a GABA receptor. The nucleic acid or DNA's encoding for a GABA receptor. The nucleic acids are also useful for the recombinant expression of D. variabilis GABA-gated chloride channel proteins. GABA-gated chloride channel proteins exert toxic effects on other ticks or related parasites such as mites. The present sequence is Dermacentor variabilis clone 8 GABA-gated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; Fig 3; 59pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptide useful for preventing or treating tick infestation, humans, dogs, cattle, horses, deer, or other wild or domesticated animals, comprises the Dermacentor variabilis gamma-aminobutyric aci (GABA)-gated chloride channel
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 MetAspLeuLysAsnPheProMetAspIleGlnThrCysThrMetGlnLeuGluSerSer
                                                                                                TTCGCCAACGAGAAGAGCGCCTACTTTCATGCGGCCACAACGCCCAACACTTTCCTCCGC
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                                                                      Dermacentor
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                                                                                                                                         GABA-gated chloride channel
                                                                                                             infestation;
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omestic animal;
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to gamma-aminobutyric acid (GABA)-gated chloride channels and their corresponding nucleic acid molecules. GABA-gated chloride channel proteins and DNA's are useful for preventing and treating tick infestation, particularly in humans, dogs, cattle, horses, deer, or other wild or domesticated animals. The nucleic acids are useful as hybridisation probes or Polymerase Chain Reaction primers for identifying the presence of Dermacentor variabilis GABA-gated chloride channel nucleic acid or DNA's encoding for a GABA receptor. The nucleic acids are also useful for the recombinant expression of D. variabilis GABA-gated chloride channel proteins expression of D. variabilis GABA-gated chloride channel proteins. The present sequence is Dermacentor variabilis clone 9 GABA-gated chloride channel proteins. The present sequence is Dermacentor variabilis clone 9 GABA-gated chloride channel proteins cated parasites such as mites. The present sequence is Dermacentor variabilis clone 9 GABA-gated chloride channel proteins cated parasites such as mites. The present sequence is Dermacentor variabilis clone 9 GABA-gated chloride channel parasites such as mites. The present sequence is Dermacentor variabilis clone 9 GABA-gated chloride channel parasites such as mites.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1614 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chloride channel DNA.
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                                                                                                                                           ---AspSerLeuAspLeuAspProSerMetLeuAspSerIleTrpLysProAspLeuPhe
                                                                                                                                                                                                                                                                                                                ACACGTGGGTACGACAGGAGGGTGAGGCCAAATTATGGCGGCGTTCCAGTGGAAGTTGGC
                                                                                                                                                                                                                                                                                                                            ThrSerGlyTyrAspAlaArgIleArgProAsnPheLysGlyProProValAsnValThr
                                                                                                                         CTCGAGAGCATGACTGTGGGCGCTGAAGTGGCCGAGAGGATCTGGGTACCCGACACCTTC
                                                            TTCGCCAACGAGAAGAGCGCCTACTTTCATGCGGCCAACACGCCCAACACTTTCCTCCGC
ATCGGCTCCGGAGGAGGAGGTTTTCCGCAGTATTCGACTGACGGTGACTGCCCAGCTGCCCA
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---GGCATCCCAAGGACAACCGAGGGAAGCACCACCAACCGGATTTAC 1241
                        {\tt ProProAlaProLeuLeuArgGluGlyGluThrThrArgLysLeuTyr}
                                                       CATTGTCAAGACGGTCGGTTCCTGTCAAGTTTGTCCTGCTGCGGT
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                                                                                                                                                                            CGCTGTCAGCAGCTGGCAAAACTTGCAGAGCAACACAGGCAGAGATG-CGCCGCAGCTTC
                                                                                                                                                                                                                                     TACGCCGCGGTAGGATATCTCGGCAAGAGA....
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                                                                                                                                                                                                                                                                                               AAGAGTATCGACGTCTACCTGGGCACATGTTTCGTAATGGTGTTTACCGCGCTCCTGGAG
                                                                                                                                                                                                                                                                                                                                                       CTCACGATGACCACACTCATGTCCAGTACCAACGCAGCGCTGCCCAAAATATCCTACGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ·-----CGCCTGGTATGT---GAAATACGGTTC-----GCCCGCTCCATG
                                                                                                                                                                                                        ------ArgGlnArgArgGlnArgLeuGluGluAspIle
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Search completed: June 30, 2003, 23:13:41 Job time : 383.186 secs

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Result
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-DB=ISSUEd_Patents_Na -QPMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DCALIGN=200 -THR_SCORE=pct -THR_MAX=1.00 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10075846_@CGN 1_1_84_@runat_25062003_163649_5167 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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-MODEL-frame+_p2n.model -DEV-xlp
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Ygapop 10.0 , 1
Fgapop 6.0 , 1
Delop 6.0 , 1
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Match
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Listing first 45 summaries
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Ygapext
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                               US-09-592-891A-13

US-09-592-891A-11

US-09-130-339-1

US-08-435-933-5

PCT-US96-06035-5

US-09-592-891A-12

US-09-002-361-1

US-08-072-064-7

US-08-072-064-7

US-08-554-659-3

US-08-554-659-3
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ALIGNMENTS

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LENGTH: 4621
TYPE: DNA
ORGANISM: Heliothis virescens
FEATURE:
NAME/KEY: unsure
LOCATION: (764)...(764)
OTHER INFORMATION: n is a, t, g
US-09-592-891A-13
                                                Best Local Similarity:
Query Match:
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US-10-075-846-4 (1-431) x US-09-592-891A-13 (1-4621)
                                                                                   Percent Similarity:
                                                                                                       Score:
                                                                                                                                     Alignment Scores:
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SOFTWARE: FastSEQ for
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Xiao-Zhou Michelle Wang
APPLICANT: Xavier Georges Sarda
APPLICANT: Michael David Tomalski
APPLICANT: Wincent Paul Mary Wingate
TITLE OF INVENTION: Heliothis Glutamate Receptor
FILE REFERENCE: A32815 072667.0118
CURRENT APPLICATION NUMBER: US/09/592,891A
CURRENT FILING DATE: 2001-01-22
                                                                                                                     No.:
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31 GluValLysSerGlyThrLysGlySerGlnProMetSerProSerAspPheLeuAspLys 50

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                                                                                                                               CTACTAGAGTTCGCGCTCGTCAACTATGCGTCTCGCTCTGACATGCACCGAGAGAACATG
                                                                                                                                                  LeuLeuGluTyrAlaAlaIleAsnPheValSerArg-----GlnHisLysGluPheIle
                                                                                                                                                                                                                           SerTyrValLysAlaIleAspIleTrpMetAlaValCysLeuLeuPheValPheAlaAla
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                                                       AAGAAAGCGAGACGGGAGATGGAAGCAGCCAGCATGGATGC-TGCCTCAGATCTCCTAGA
                                                                                           ArgLeuArgArgArgGlnArgArgGlnArgLeuGluGluAspIleIleGlnGluSerArg
                                                                                                                                                                                                        TCCTACACGAAAGCCATTGACGTCTGGACTGGTGTATGTCTCACATTCGTATTCGGAGCG
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Best Local Similarity:
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OTHER INFORMATION:
US-09-592-891A-11
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SOFTWARE: FastSEQ for
SEQ ID NO 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Xiao-Zhou Michelle Wang
APPLICANT: Xavier Georges Sarda
APPLICANT: Michael David Tomalski
APPLICANT: Winchael David Tomalski
APPLICANT: Vincent Paul Mary Wingate
TITLE OF INVENTION: Hellothis Glutamate Receptor
FILE REFERENCE: A32815 072667.0118
CURRENT APPLICATION NUMBER: US/9/592,891A
CURRENT FILING DATE: 2001-01-22
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                                                                                                                                                                                                                                                                                                                                                                    88 ThrThrMetAspTyrArgValAsnValPheLeuArgGlnGlnTrpAsnAspProArgLeu 107
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                                                                                                                               AspAsnLysLeuLeuArgIlePheLysAsnGlyAsnValLeuTyrSerIleArgLeuThr 167
                                                                                                                                                                                                                                                             GTCACAATGGAATACTCCGTACAATTAACGTTTCGGGAACAATGGTTAGATGAACGGCTC
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                                      CTGACGCTCTCGTGCCCCATGAACCTCAAGTTGTACCCCCTGGATAAGCAGACCTGCTCG
                                                         LeuIleLeuSerCysLeuMetAspLeuLysAsnPheProMetAspIleGlnThrCysThr 187
                                                                                                                                                                                                                                                                                               SerTyrArgGluTyrProAspAspSerLeuAspLeuAspProSerMetLeuAspSerIle 127
                                                                                                                                                                                                                                                                                                                                                                                                            GATGGGCCAGCGGTAGTGAGCGTCAATATATTTGTCCGAAGTATATCAAAGATCGATGAC
 MetGlnLeuGluSerSerSerIleLeuCysSerProLeuProSerLeuSerLeuSerVal
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; SEO ID NO 1 ; LENGTH: 1368 ; TYPE: DNA ; ORGANISM: ctenocephalides felis US-09-130-339-1 Alignment Scores:	NO. 1		Db 688 CTCAGGATG
Q D Q D Q D Q	Q	Q D Q D Q D Q	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
GTYCCGGCCAGAGTATCACTGGGTGTGACCACTCTCCTCACCATGGCCACCACGAGGTCGGGCCAGAGTATCACTGGGTGTGACCACTCCTCACCATGGCCACCACAGGCCACCCAGACGTCGGCTCGGCCACCAGACGTCGGGTGTGACCACTCCTCCACCATGGCCACCCAGACGTCGGGTGTGACCACTAGAGGCACCAGAGGCACCAGAGGCACCAGAGAGGCACCAGAGAGGCACCAGAGAGGCACCAGTGTACAGAGAGAG	219 LeuGluAspAlaProAlaValGlnValAlaGluGlyLeuThrLeuProGlnPheIleLeu 238	119 LeuAspProSerMetLeuAspSerIleTrpLysProAspLeuPhePheAlaAsnGluLys 138	24 ArgvalalaLeualaLysGluGluValLysSerGlyThrLysGlySerGlnProMetSer 43

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                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,933
FILING DATE:
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (908) 594-47ZU INFORMATION FOR SEQ ID NO: 5 SEQUENCE CHARACTERISTICS: LENGTH: 3958 base pairs
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No.:
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NAME: Wallen, III John W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 19264
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: John W. Wallen III
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STATE: New Jersey
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TOPOLOGY: lir
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ZIP: 07065-0907
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                   ArgPro-----AsnPheLysGlyProProValAsnValThrCysAsnIlePheIle 79
                                                                                     AAGGAGAAAAAGTCTTAGATCAAATTTTAGGT----GCAGGCAAATACGACGCCCGAATA
                                                                                                                     SerProSerAspPheLeuAspLysLeuMetGlyArgThrSerGlyTyrAspAlaArgIle 62
                                                                                                                                                        TACTTTGCCAGCCTGTGCAGTGCTTCACTAGCAAATAATGCCAAGGTAAATTTCCGAGAA
                                                                                                                                                                                                                                                        ThrLeuValProAlaThrLeuSerPheLeuLeuLeuTrpThrLeuProGlyGlnValLeu 22
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Arena, Joseph P.
Paress, Philip S.
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APPLICANT: Paress, APPLICANT: Liu, Ker TITLE OF INVENTION:
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APPLICANT:
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                                                                                                     Application PC/TUS9606035
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                                                                                                                                                                                                                                                                                                          GTGTCTGACGTTCGTGTTCGGGGCCCTGCTCGAGTTCGCCCTGGTGAACTATGCATCCCG 140:
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                                                                                                                                                                                                                                          ATCAGGTTCGAATAAAGCTAACATGCATAAGGAGAATATGAAAAAGAAGCGCCGCGATCT 1462
               Cully, Doris F.
Arena, Joseph P.
Paress, Philip S.
Liu, Ken K.
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DNA ENCODING GLUTAMATE GATED CHLORIDE
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US-10-075-846-4 (1-431) x PCT-US96-06035-5 (1-3958)
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Best Local Similarity:
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MOLECULE TYPE:
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REFERENCE/DOCKET NUMBER: 19264 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06035
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NAME: Glesser, Jody M.
REGISTRATION NUMBER: 32,
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MEDIUM TYPE: Floppy disk
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CLASSIFICATION:
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Conservative:
Mismatches:
Indels:
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                                                                      NUMBER OF SEQ ID NOS:
SOFTWARE: FASTSEQ FOI
SEQ ID NO 12
LENGTH: 1640
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                         US-09-592-891A-12
                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Xiao-zhou michelle Wang
APPLICANT: Xiao-zhou michelle Wang
APPLICANT: Xivier Georges Sarda
APPLICANT: Michael David Tomalski
APPLICANT: Vincent Paul Mary Wingate
TITLE OF INVENTION: Heliothis Glutamate Receptor
FILE REFERENCE: A32815 072667.0118
CURRENT APPLICATION NUMBER: US/09/592,891A
CURRENT FILING DATE: 2001-01-22
                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/09592891A Patent No. 6329174
OTHER INFORMATION: PCR amplified fragment of Heliothis DNA cloned OTHER INFORMATION: into pCR2.1-TOPO vector (Invitrogen)
                                      FEATURE:
                                                     ORGANISM: Artificial Sequence
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                                                                                                                              FastSEQ for Windows Version
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Best Local Similarity:
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ValSerTyrValLysAlaIleAspIleTrpMetAlaValCysLeuLeuPheValPheAla
                                   GTGACGACTTTACTTACAATGGCGACCCAGTCGTCAGGCATCAACGCGTCCCTACCACCG
                                                         IleThrThrValLeuThrMetThrThrGlnSerSerGlySerArgAlaSerLeuProLys 325
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                                                                                                     GTGTCCTGGGTGTCCTTCTGGCTGGACCAGGGAGCTGTGCCTGCGAGGGTCTCACTAGGA
                                                                                                                       LeuSerTrpValSerPheTrpIleAsnMetAspAlaAlaProAlaArgValGlyLeuGly 305
                                                                                                                                                                         AAACGCGAGTTCAGTTACTACCTGATCCAGATCTACATTCCGTGCTGCATGCTGGTCATC
                                                                                                                                                                                           GluArgGlnMetGlyTyrTyrLeuileGlnMetTyrIleProSerLeuLeuileValile 285
                                                                                                                                                                                                                                              TACTGCAACAGTAAGACTAATACCGGTGAATACAGTTGCCTGAAGGTAGACCTGCTCTTC
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gTCTGGATGCCTGATCTATTCTTCTCCAACGAGAAGGTCATTTCCACAACATCATC 510
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Query Match:
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US-09-002-361-1
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                                                    US-10-075-846-4 (1-431) x US-09-002-361-1 (1-1844)
                                                                                                                              Percent Similarity:
                                                                                                                                             Score
                                                                                                                                                                         Alignment Scores:
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert_Price
                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Halling, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 609-520-3214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                            Мо
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LOCATION:
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SOFTWARE: FastSEC
                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                         TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Lawrenceville
                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                        LeuProGlyGlnValLeuLeuArgValAlaLeuAlaLysGluGluValLysSerGlyThr
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                                                                                                                                 ACGGTTGGCTATATGGCTAAA---
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                                                                                    ArgGlnArgLeuGluGluAspIleIleGlnGluSerArgPheTyrPheArgGlyTyrGly 391
LeuGlyHisCysLeuGlnAlaArgAspGlyGlyProMetGluGlySerGlyIleTyrSer 411
                                            AGATTCACTGCTGTTCAAAAAATGGCCGCCGAGAAGAAAATGCAAATA------
                                                                                                                              AGGATACAGATGAGGAAACAA
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US-10-075-846-4 (1-431) x US-08-072-064-7 (1-2066)
                                                                                                                          Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 770,881
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-00
                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEYELICANT: JACKSON, MEYER B.
TITLE OF INVENTION: DRUG AND PESTICIDE SCREENING NUMBER OF SEQUENCES: 20
CORRESPONDENCE: 20
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MEDIUM TYPE: Floppy of COMPUTER: IBM PC COM
                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 2066 base pair
                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
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ADDRESSEE: PETER G. CARROLL
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STATE: California
                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                     TYPE: NUCLEIC ACID
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: U: FILING DATE: 19930602
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                 AATCCCAATCCCAATGCAAATGTGGGCGGACCC---GGAGGAGTGGGCGTTGGACCCGGC 1312
                                                                                                 ATCCAAAAGATAGCCGAACAGAAAAAAGCAACAGCTCGACGGAGCGAACCAACAGCAGGCG
                                                                                                                                       GluGluAspIleIleGlnGluSerArgPheTyrPheArgGlyTyrGlyLeuGlyHisCys
                                                                                                                                                                                                                     ValSerArgGlnHisLysGluPheIleArgLeuArgArgGlnArgArgGlnArgLeu
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                                                 -LeuGlnAlaArgAspGlyGlyProMetGluGlySerGlyIIeTyrSerPro
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                          Score:
                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/002,361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Halling, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: PRIOR APPLICATION DATA:
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ZIP: 08543
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Lawrenceville
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OTHER INFORMATION:
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997 Lenox Drive, Building
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Conservative:
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                                         GACATAAGCAAACTG 1296
                                                                        ThrThrArgLysLeu 428
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Best Local Similarity:
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Patent No. 5767361
GENERAL INFORMATION:
APPLICANT: Wingate, Vincent
APPLICANT: Wolff, Mark
TITLE OF INVENTION: LEPIDOPTERAN GABA GATED CHLORIDE
TITLE OF INVENTION: AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: DIGIGIO, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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LENGTH: 1657 base pairs
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CITY: Garden City
STATE: New York
COUNTRY: USA
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                                                                                                                             GTAAGCTACGACAAAAGAGTGAGGCCGAACTATGGAGGACCGCCAGTGGATGTGGGAGTC
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                                                                                       GlnAlaArgAspGlyGlyProMetGluGlySerGlyIleTyrSerProGlnProProAla
                                                                                                                                                                                      ATCCCCCCACCGAGGACCAGCACCCTATCTAGGCCACCACCTAGCCGATTATCGGAGGTT 127
                                                                                                                                                                                                                                                                               Argarg....-GlnArgLeuGluGluAsp.....
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Best Local Similarity:
Query Match:
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; LOCATION:
US-08-554-659-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (516).742-4343
TELEPAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 3:
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NERAL INCOMP.

APPLICANT: Wingate, Vincent

APPLICANT: Wolff; Mark

APPLICANT: Wolff; Mark

TITLE OF INVENTION: AND METHODS OF USE THEREOF

TITLE OF INVENTION: AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S
REGISTRATION NUMBER: 31,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1657 base pair
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: sing
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ZIP: 11530-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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                                                                       LeuProGlyGlnValLeuLeuArgValAlaLeuAlaLysGluGluValLysSer----Gly
                             ValPheLeuArgGlnGlnTrpAsnAspProArgLeuSerTyrArgGluTyrProAsp---
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                                                                                                                                   GTAAGCTACGACAAAAGAGTGAGGCCGAACTATGGAGGACCGCCAGTGGATGTGGAGTC
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                SerGlyTyrAspAlaArgIleArgProAsnPheLysGlyProProValAsnValThrCys 75
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Conservative:
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RESULT 12
US-08-072-064-2
; Sequence 2, Application US/08072064
; Patent No. 6008046
; GENERAL INFORMATION:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 770,881
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/705-8410
TELEFAX: 415/397-8338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: JACKSON, MEYER B.
TITLE OF INVENTION: DRUG AND PESTICIDE SCREENING
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETER G. CARROLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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            Sequence 3, Application US/08072064
Patent NO. 6008046
GENERAL INFORMATION:
APPLICANT: FFRENCH-CONSTANT, RICHARD
APPLICANT: JACKSON, MEYER B.
TITLE OF INVENTION: DRUG AND PESTICID
 NUMBER
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SEQUENCES:
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DRUG AND PESTICIDE 20
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Query Match:
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REFERENCE/DOCKET NUMBER: OPHD
TELEPHONE: 415/705-8410
TELEPHONE: 415/797-8338
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2066 base pairs
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APPLICATION NUMBER: US/(
TTIME DATE: 1990602
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ADDRESSEE: PETER G. CARROLL
STREET: 220 Montgomery Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 770,881
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
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TOPOLOGY: un
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CITY: San Francisco
STATE: California
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                          SerLeuAspLeuAspProSerMetLeuAspSerIleTrpLysProAspLeuPhePheAla 135
                                                                                                       PheLeuArgGlnGlnTrpAsnAspProArgLeuSerTyrArgGluTyrProAsp----Asp 115
                                                                                                                                                                                        IlePheIleAsnSerPheSerSerValThrLysThrThrMetAspTyrArgValAsnVal
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              ACACTATCGGTTGGATCAGAGTTCATTAAGAATATTTGGGTACCTGACACCTTTTTTGTA 538
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Sequence 5, Application US/08072064
Patent No. 6008046
GENERAL INFORMATION:
APPLICANT: FFRENCH-CONSTANT, RICHARD H.
APPLICANT: JACKSON, MEYER B.
TITLE OF INVENTION: DRUG AND PESTICIDE SC
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: PETER G. CARROLL
STREET: 220 Montgomery Street, Suite 22
CITY: San Francisco
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: OF TELECOMMUNICATION INFORMATION: 115/705-8410
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APPLICATION NUMBER: US
FILING DATE: 19930602
CLASSIFICATION: 435
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LENGTH: 2066 base pair
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ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: CARROLL, PETER G. REGISTRATION NUMBER: 32,837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 770,881
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AGTTACGACAAAAGAGTAAGACCCAATTACGGTGGTCCCCCTGTGGAGGTTGGCGTCACA 358
                                        AsnGluLysGlyAlaAsnPheHisGluValThrThrAspAsnLysLeuLeuArgIlePhe 155
                                                                                                              SerLeuAspLeuAspProSerMetLeuAspSerIleTrpLysProAspLeuPhePheAla 135
                                                                                                                                                                                      PheLeuArgGlnGlnTrpAsnAspProArgLeuSerTyrArgGluTyrProAsp---Asp 115
                                                                                                                                                                                                                                                               GGCGGTGGCAGCATGCTGGGTGACGTAAACATATCCGCTATTCTCGACTCCTTTAGTGTT
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                     AATGAAAAACAATCATATTTTCACATTGCAACAACCAGTAATGAATTCATACGTGTGCAT
                                                                                                                                                                  TACTTTCGTCAATTTTGGACCGATCCTCGTTTAGCGTATAGAAAACGACCTGGTGTAGAA
                                                                                                                                                                                                                                            ATGTATGTCCTCAGTATCAGTTCGGTTTCGGAAGTTCTAATGGACTTCACATTGGATTTT 418
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RESULT 15
US-08-137-614A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Gene Encoding An Insect
TITLE OF INVENTION: Gamma-Aminobutyric Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Soderlund, David M. APPLICANT: Knipple, Douglas C. APPLICANT: Henderson, Joseph E.
                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                 STREET: Clinton
CITY: Rochester
                                                                                                                                                                                                                                            COUNTRY:
         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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||| ::: ||||||||||::::||||||||::::::
ATGTCGTCAACAAATGCAGCGCTGCCAAAGATTTTCGTACGTCAAATCGATTGACGTCTAT 109
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ATCTACATACCCTCTGGACTGATCGTTATATCATGGGTATCATTTTGGCTCAATCGC 973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGGCAAAACGAATTCAAATACGAAAACAAAGATTTATGGCGATCCAAAAGATAGCCGAA 1213
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                                                                                                                                                                                                                                                                           New York
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                                                                                                                                                                                                                                            USA
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; MOLECULE TYPE:
US-08-137-614A-3
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NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716)263-1636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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CLASSIFICATION:
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ThrMetLysAspLeuValPheGluTrpLeuGluAspAlaProAlaValGlnValAlaGlu
                                                                                                                                                                              CTCGCCTGCATGATGGATCTGCACTACTATCCATTGGACTCGCAGAATTGCACTGTGGAA 579
                                                                                                                                                                                                             LeuSerCysLeuMetAspLeuLysAsnPheProMetAspIleGlnThrCysThrMetGln
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379 IleIleGlnGluSerargPheTyrPheArgGlyTyrGly 391 	9 IleIleGlnGluSerArg 3 GACGTGTTCAACGACAGA	Qy . 379 Db 1113
GlnHisLysGluPheIleArgLeuArgArgGlnArgArgGlnArgLeuGluGluAsp 378 ::::::		Оу 359 Db 1053
AlaAlaLeuLéuGluTyrAlaAlaIleAsnPhe		Qy 345 Db 994
LysValSerTyrValLysAlaIleAspIleTrpMetAlaValCysLeuLeuPheValPhe::::::		Qy 325 Db 934
GlyIleThrThrValLeuThrMetThrThrGlnSerSerGlySerArgAlaSerLeuPro		Qy 305 Db 874
IleLeuSerTrpValSerPheTrpIleAsnMetAspAlaAlaProAlaArgValGlyLeu:::		Qy 285 Db 814
LeuGluArgGlnMetGlyTyrTyrLeuIleGlnMetTyrIleProSerLeuLeuIleVal ::: :::		Qy 265 Db 754
GlyCysCysThrLysHisTyrAsnThrGlyLysPheThrCysIleGluValLysPheHis 264	Glycysc	Qy 245 Db 709
GlyLeuThrLeuProGlnPheIleLeuArgAspGluLysAspLeu 244		Oy 230 Db 652
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Search completed: July 1, 2003, 00:57:28 Job time: 115.6 secs

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Command line parameters:

MODEL-frame+_p2n.model -DEV-xlp

-Q-cgn2_1/USPTO_spool_VS10075846/runat_25062003_163649_5181/app_guery.fasta_1.782

-Q-cgn2_1/USPTO_spool_VS110075846/runat_25062003_163649_5181/app_guery.fasta_1.782

-DB-Published_Applications_NA -QFMT-fastap -SUFFIX-p2n.rnpb -MINMATCH=0.1

-LOOPEXT-0 -UNITS-blits -START-1 -END--1 -MATRIX-blosum62

-TRANS-human40.cd1 -LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MX=100

-THR_MIN-0 -ALIGN-15 -MODE-LOCAL -QUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0

-MAXLEN-200000000 -USER-US10075840_4CGN_11_102_grunat_25062003_163649_5181

-NCPU-6 -ICPU-3 -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLOCK-100

-LONGLOG -DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5

-FGAPOP-6 -FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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                                                                                                                   Score
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/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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                                                                   GluLysAspLeuGlyCysCysThrLysHisTyrAsnThrGlyLysPheThrCysIleGlu
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TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A:
TITLE OF INVENTION: IN THE GASTROINTESTINAL TR.
FILE REFERENCE: D0079 NP
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: US/10/075,846
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: US 60/289,535
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 2565
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; LOCATION: (1)..(1251)
US-10-075-846-1
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                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: homo
                                                                                                                                                                                                                                                                             FEATURE:
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TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL GLYCINE RECEPTOR ALPHA SUBUNI
TITLE OF INVENTION: IN THE GASTROINTESTINAL TRACT, HGRA4, and SPLICE VARIANT THER
FILE REFERENCE: D0079 NP
CURRENT PILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: US/10/075,846
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: US 60/269,535
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
LENGTH: 993
TYPE: AND THE PRIOR PRIOR PRIOR PATENTING PATENTANG PATENTING PATENTING PATENTING PATENTING PATENTING PATENTING 
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68 GlyProProValAsnValThrCysAsnIlePheIleAsnSerPheSerSerValThrLys	⊷ o	Qy 31 GluValLysSerGlyThrLysGlySerGlnProMetSerProSerAspPheLeuAspLys 50	33.30% Indels: 9 Gaps: 1) x US-09-969-844-13 (1-4621)	Pred. No.: 6.99e-85 Length: 4621 Score: 750.00 Matches: 167 Percent Similarity: 58.42% Conservative: 62 Best Local Similarity: 42.60% Mismatches: 139		; ORGANISM: Heliothis virescens ; FEATURE: ; NAME/KEY: unsure ; LOCATION: (764)(764)	SOFTWARE: FastSEQ for SEQ ID NO 13 LENGTH: 4621 TYPE: DNA	FILE REFERENCE: A32815-I 072667.0178 CURRENT APPLICATION NUMBER: US/09/969,84 CURRENT FILING DATE: 2001-10-03 NUMBER OF SEQ ID NOS: 14	; APPLICANT: Xavier Georges Sarda ; APPLICANT: Michael David Tomalski ; APPLICANT: Vincent Paul Mary Wingate ; TITLE OF INVENTION: Heliothis Glutamate Receptor	0 = 0	RESULT 4 US-09-969-844-13	Oy 321 AlaSerLeuProLys 325	919 CGTGTGGGCATCACCACCGTGCTCACCATGACCACCCAGAGCTCTGGCTCCCGG	Db 859 CTACTCATCGTCATCCTGTCCTGGGTCTCCTTCTGGATCAACATGGATGCTGCCCTGCCC 918 OV 301 ArgValGlvIeuGlvTleThrThrVallenThrMetThrThrGlnSerSerGlvSerArg 320	281 LeuLeuIleValIleLeuSerTrpValSerPheTrpIleAsnMetAspAlaAlaProAla	Qy 261 ValLysPheHisLeuGluArgGlnMetGlyTyrTyrLeuIleGlnMetTyrIleProSer 280	Qy 241 GluLysAspLeuGlyCysCysThrLysHisTyrAsnThrGlyLysPheThrCysIleGlu 260	679 GATGCTCCTGCCCAAGTGGCTGAGGGGCTGACTCTGCCCCAGTTTATCTTGCGGGAT	Db 634AGCTTTGGCTACACCATGAAAGACCTCGTGTTTGAGTGGCTGGAA 678 Ov 221 AspAlaProAlaValGlnValAlaGluGlvLeuThrLeuProGlnPheTleLeuArgasn 240
RESULT 5 US-09-969-844-11 ; Sequence 11, Application US/09969844 ; Publication No. US20020192776A1	Qy 405 GluGlySerGlyIleTyrSerProGlnProProAla 416 ::: :::	Oy 385 PheTyrPheArgGlyTyrGlyLeuGlyHisCysLeuGlnAlaArgAspGlyGlyProMet 404 ::: :::	Qy: 365. ArgLeuArgArgArgGlnArgArgGlnArgLeuGluAspIleIleGlnGluSerArg 384 ::: :::::::::::::::::::::::::::::::::	Qy 347 LeuLeuGluTyrAlaAlaIleAsnPheValSerArgGlnHisLysGluPheIle 364	Qy 327 SerTyrValLysAlaIleAspIleTrpMetAlaValCysLeuLeuPheValPheAlaAla 346	Qy 307 ThrThrValLeuThrMetThrThrGlnSerSerGlySerArgAlaSerLeuProLysVal 326	Qy 287 SerTrpValSerPheTrpIleAsnMetAspAlaAlaProAlaArgValGlyLeuGlyIle 306	Qy 267 ArgGlnMetGlyTyrTyrLeuIleGlnMetTyrIleProSerLeuIleValIleLeu 286 :::	Qy 247 CysThrLysHisTyrAsnThrGlyLysPheThrCysIleGluValLysPheHisLeuGlu 266	Oy . 228 AlaGluGlyLeuThrLeuProGlnPheIleLeuArgAspGluLysAspLeuGlyCys 246	Db 702 GGTTGGACCACAGACGACTTAGTGTTCCTATGGAAGGCGACCCGGTGCAGGTG 758	684 CTCAGGATGGCTAGTTAT	Qy 188 MetGlnLeuGluSerSerSerIleLeuCysSerProLeuProSerLeuSerLeuSerVal 207	168 LeuIleLeuSerCysLeuMetAspLeuLysAsnPheProMetAspIleGlnThrCysThr	564 CCGAACGTGTACATCCGGATCTTCCCCAACGGCAACGTGCTGTACAGCATCCGAATCTCC	Db 504 TGGATGCCTGATCTATTCTTCTCCAAGAAGGAAGGTCATTTCCACAACATCATCATG 563 Oy 148 AspAsnLysLeuLeuArgIlePheLysAsnGlyAsnValLeuTyrSerIleArgLeuThr 167	. Db 444 AAATTCAATAATCTTGGAGGTCGCCTCAAATACCTGACACTGACCGAAGCCAACAGAGTC 503 Qy 128 TrpLysProAspLeuPhePheAlaAsnGluLysGlyAlaAsnPheHisGluValThrThr 147		88 ThrThrMetAspTyrArgValAsnValPheLeuArgGlnGlnTrpAsnAspProArgLeu ::: :::

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GENERAL INFORMATION:
APPLICANT: X100-Zhou Michelle Wang
APPLICANT: Xavier Georges Sarda
APPLICANT: Michael David Tomalski
APPLICANT: Michael David Tomalski
APPLICANT: Vincent Paul Mary Wingate
APPLICANT: Vincent Paul Mary Wingate
TITLE OF INVENTION: Heliothis Glutamate Receptor
FILE REFERENCE: A32815-I 072667.0178
CURRENT APPLICATION NUMBER: US/09/969,844
CURRENT FILING DATE: 2001-10-03
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 11
LENGTH: 1609
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                                                                          GlyTyrThrMetLysAspLeuValPheGluTrpLeuGluAspAlaProAlaValGlnVal
                                                                                                                               MetGlnLeuGluSerSerSerIleLeuCysSerProLeuProSerLeuSerLeuSerVal
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                         AlaGluGlyLeuThrLeuProGlnPheIleLeuArgAspGluLysAspLeu---GlyCys
                                                   GGTTGGACCACAGACGTTAGTGTTCCTATGGAAGGAAGGCGACCCG---GTGCAGGTG
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US-10-075-846-4 (1-431) x US-10-239-420-10 (1-1197)
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Best Local Similarity:
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APPLICANT: Cully, Doris F.

APPLICANT: Zheng, Yingcong

TITLE OF INVENTION: DNA MOLECULES ENCODING LIGAND GATED ION

TITLE OF INVENTION: CHANNELS FROM DERMACENTOR VARIABILIS

FILE REFERENCE: 20629p

CURRENT APPLICATION NUMBER: US/10/239,420

CURRENT FILING DATE: 2001-09-23

PRIOR APPLICATION UNMBER: PCT/US01/09956

PRIOR FILING DATE: 2001-03-28

PRIOR FILING DATE: 2001-03-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/193,935
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 10
LENGTH: 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/10239420 Publication No. US20030096984A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Rhipicephalus
                                                                                                                                                   7 TTGGACAGCATCATTGGCCAG----GGTCGTTATGACTGCAGGATCCGGCCCATGGGAATT
SerValThrLysThrThrMetAspTyrArgValAsnValPheLeuArgGlnGlnTrpAsn ::: ||||||||
                                                                                                        ---AsnPheLysGlyProProValAsnValThrCysAsnIlePheIleAsnSerPheSer
                                                                                                                                                                            LeuAspLysLeuMetGlyArgThrSerGlyTyrAspAlaArgIleArgPro------
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RESULT 7

US-09-969-844-12

Sequence 12, Application US/09969844

Publication No. US20020192776A1

GENERAL INFORMATION:
APPLICANT: Xiao-Zhou Michelle Wang
APPLICANT: Xiao-Zhou Michelle Wang
APPLICANT: Wichael David Tomalski
APPLICANT: Winchael David Tomalski
APPLICANT: Wincent Paul Mary Wingate
TITLE OF INVENTION: Heliothis Glutamate Rec
TITLE REFERENCE: A32815-I 072667.0178
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                                                                                                                                                                                                                                AspIleIleGlnGluSerArgPheTyrPheArgGlyTyrGlyLeuGlyHis 394
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                                                                                                                                                                                                                                                                                          PheIleArgLeuArgArgGlnArgArgGln------ArgLeuGluGlu
                                                                                                                                                                                                                                                                                                                           GTATTCGGCGCGCTCCTCGAGTTCGCCCTGGTCAACTACGCCTCGCGGTCAGATTCACGC
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CURRENT FILING DATE: 2001-10-03
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
LENGTH: 1640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: PCR amplified fragment of Heliothis DNA
OTHER INFORMATION: into pCR2.1-TOPO vector (Invitrogen)
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                       GluArgGlnMetGlyTyrTyrLeuIleGlnMetTyrIleProSerLeuLeuIleValIle
                                                                                                                                                                                                                                                                                                                                                                                                                             ValGlyTyrThrMetLysAspLeuValPheGluTrpLeuGluAspAlaProAlaValGln
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                                                                                    CysCysThrLysHisTyrAsnThrGlyLysPheThrCysIleGluValLysPheHisLeu
                                                                                                                            GTGGTGAAAAACTTACACCTGCCTCGGTTCACGCTG-----GAGAAGTTCCTCACTGAC
                                                                                                                                            ValAlaGluGlyLeuThrLeuProGlnPheIleLeuArgAspGluLysAspLeu---Gly
                                                                                                                                                                                        TCGCTCAGGATG:
                                                                                                                                                                                                                                                                             ThrMetGlnLeuGluSerSerSerIleLeuCysSerProLeuProSerLeuSerLeuSer
                                                                                                                                                                                                                                                                                                                           ThrLeuIleLeuSerCysLeuMetAspLeuLysAsnPheProMetAspIleGlnThrCys
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	RESULT	
1090 GCAAAGAATG 1099	Db	Db 100
372 gGlnArgLeu 375	Qy	24 ArgValblatonAlatusCluCluValtusCorolumbatusCluCoxClamaDatatos 4
**************************************	Db	Oy 4 LeuValProAlaThrLeuSerPheLeuLeuLeuTrpThrLeuProGlyGlnValLeuLeu 23
PheVal-SerArqGlnHisLvsGluPheIleArqLeuArqArqGlnArqAr	O _V	US-10-075-846-4 (1-431) x US-09-815-925-10 (1-1467)
335 TrpMetAlaValCysLeuLeuPheValPheAlaAlaLeuLeuGluTyrAlaAlaIleAsn 354 ::::::	Qу	32.26% Indels: 10 Gaps:
315 GlnSerSerGlySerArgAlaSerLeuProLysValSerTyrValLysAlaIleAspIle 334 ::::::: ::: :::	Db	rred. No.: 1.06e-82 Length: 1467 Score: 726.50 Matches: 157 Percent Similarity: 58.59% Conservative: 68 Best Local Similarity: 40.89% Mismatches: 111
	Db	lignment Scores:
295 MetAspAlaAlaProAlaArgValGlyLeuGlyIleThrThrValLeuThrMetThrThr 314	Qy	LOCATION: S-09-815-925-
275 GlnMetTyrileProSerLeuLeuIleValIleLeuSerTrpValSerPheTrpIleAsn 294 ::: :::	Оy	; TYPE: DNA ; ORGANISM: Homo sapiens ; FEATURE: ; NAME/KEY: CDS
255 LysPheThrCysIleGluValLysPheHisLeuGluArgGlnMetGLyTyrTyrLeuIle 274 ::: ::: ::: :::	Db	SOFTWARE: pt_Ft_genes Version 2.0 SEQ ID NO 10 LENGTH: 1467
3 CAGTTCTCCATCGTGGAGCACCGTCTGGTCTCGAGGAATGTTGTCTTCGCCACAGGT	Db	PRIOR
235 GlnPheIleLeuArgAspGluLysAspLeuGlyCysCysThrLysHiSTyrAsnThrGly 254	Qy	
613 GAGTTTTACTGGCGAGGCGGGGACAAGGCTGTTACCGGAGTGGAAAGGATTGAGCTCCCG 672	Db	CURRE
AGCTATGGCTACACCACGGATGACATT 6) D	FITTLE OF INVENTION: No. US20020127199Alel Nucleic Acids and
IleLeuCysSerProLeuProSerLeuSerLeuSerValGlyTyrThrMetLysAspLeu 2	Qy	APPLI
175 AspLeuLysAsnPheProMetAspIleGlnThrCysThrMetGlnLeuGluSerSerSer 194 ::::::	ОУ	: APPLICANT: Zhou, Ping ; APPLICANT: Goodrich, Ryle ; APPLICANT: Asundi, Vinod ; APPLICANT: Yang, Yonghong
CACCCTGATGGGACAGTGCTGTATGGGCTCAGAATCACCACGACAGCATGCAT	Db	GENERAL INF
155 PheLysAsnGlyAsnValLeuTyrSerIleArgLeuThrLeuIleLeuSerCysLeuMet 174	Qy	Sequence 10, Application US/09815925 ; Patent No. US20020127199A1
415 TTAAATGACAAAAAGTCATTTGTGCATGGAGTGAACAGTGAAAAACCGGATGATCCGTCTT 474	Db	RESULT 8 US-09-815-925-10
135 AlaAsnGluLysGlyAlaAsnPheHisGluValThrThrAspAsnLysLeuLeuArglle 154	Qy	Db 1120 ATGAAGAAGCGAGACGGGAG 1140
355 CTCAACCTCACGCTTGACAATCGAGTGGCTGACCAGCTATGGGTGCCCGACACATATTTC 414	DЪ	gLeuArg
115 AspSerLeuAspLeuAspProSerMetLeuAspSerIleTrpLysProAspLeuPhePhe 134	Qy	Db 1060 GCGCTACTAGAGTTTGCGCTCACTATGCGTCTCGCTCTGACATGCACCGAGAGAAC 1119
298 ACCATGTATTTTCAACAATATTGGAGAGAGATAAAAGGCTCGCCTATTCTGGGATCCCT 354	Db	AlaIleAsnPheValSerArgGlnHisI
	Qy	Db 1000 GTGTCCTACACGAAAGCCATTGATGTCTGGACTTGGGTTATGTCTCACATTCGTATTCGGA 1059
	Db .	326 ValSerTyrValLysAlaIleAspIleTrpMetAlaValCysLeuLeuPheValPheAla
181AAAGGCTACGACATTCGCCTAAGACCCGACTTCGGGGGTCCCCCGGTCTCCGTGGGG 237 75 CvsAsnIleDheIleAsnSerPheSerSerValThrLvsThrThrMetAspTvrArqVal 94	0 b	qy 300 lethrinyalleurnrmetrinfidinserserglyseragalaserleubrolys 325
55 ThrSerGlyTyrAspAlaArgIleArgProAsnPheLysGlyProProValAsnValThr	Qy	880 GTGTCCTGGGTGTCCTTCTGGCTGGACCAGGGAGCTGTGCCTGCGAGGGTCTCACTAGGA
7 GTGAACGATCCCGGGAACATGTCCTTTGTGAAGGAGAGGTGGACAAGCTGTTG	Db	286 LeuSerTrpValSerPheTrpIleAsnMetAspAlaAlaProAlaArgValGlyLeuGly
44 ProSerAsp	Qy	Db 820 AAACGCGAGTTCAGTTACCTGATCCAGATCTACATTCCGTGCTGCATGCTGGTCATC 879

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Sequence 3, Application US/10239420

Publication No. US20030096984A1

GENERAL INFORMATION:

APPLICANT: Cully, Doris F.

APPLICANT: Zheng, Yingcong

TITLE OF INVENTION: DNA MOLECULES ENCODING LIGAND GATED ION

TITLE OF INVENTION: CHANNELS FROM DERMACENTOR VARIABILIS

FILE REFERENCE: 20629P

CURRENT APPLICATION NUMBER: US/10/239,420

CURRENT FILING DATE: 2002-09-23

PRIOR APPLICATION NUMBER: PCT/US01/09956

PRIOR FILING DATE: 2001-03-35

PRIOR APPLICATION NUMBER: 60/193,935

PRIOR APPLICATION NUMBER: 60/193,935

PRIOR APPLICATION NUMBER: 500/193,935

PRIOR FILING DATE: 2000-03-31

NUMBER OF SEQ ID NOS: 13

SOFTMARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 3442
TYPE: DNA
ORGANISM: Dermacentor variabilis
FEATURE:
                                                                                                                               416 GAGTTCCAATATGTCACAGTACCTAATGTACTGGTCCGCGTTAACCCGAACGGAAAGATT
                                                                       LeuTyrSerIleArgLeuThrLeuIleLeuSerCysLeuMetAspLeuLysAsnPhePro
                                                                                                                                                                                                                                                             ProSerMetLeuAspSerIleTrpLysProAspLeuPhePheAlaAsnGluLysGlyAla
                                                                                                                                                                       AsnPheHisGluValThrThrAspAsnLysLeuLeuArgIlePheLysAsnGlyAsnVal
                                                                                                                                                                                                                                                                                                                                  AspProArgLeuSerTyrArgGluTyrProAspAspSer-----LeuAspLeu---Asp 120
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  MetAspIleGlnThrCysThrMetGlnLeuGluSerSerSerIleLeuCysSerProLeu
                                            CTATACATGCTCAGGCTCAAGCTAAGGTTTGCATGTATGGATCTATATCGCTTTCCT
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                                                                                                                                                                                                                                                                                                            GATGATCGCTTGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGGATGACCTGGAGAAGCTTGACGACTTATTAAGAACCTATGACCGGCGTGCCCTTCCC
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                                          US-10-075-846-4 (1-431) x US-10-239-420-1 (1-3598)
                                                                                                         Query Match:
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Best Local Similarity:
                                                                                                                                                                       Score:
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                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                               US-10-239-420-1
                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/239,420
CURRENT FILING DATE: 2002-09-23.
PRIOR APPLICATION NUMBER: PCT/US01/09956
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: 60/193,935
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 1
LENGTH: 3598
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10239420 Publication No. US20030096984A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cully, Doris F.
APPLICANT: Zheng, Yingcong
TITLE OF INVENTION: DNA MOLECULES ENCODING LIGAND GATED IC
TITLE OF INVENTION: CHANNELS FROM DERMACENTOR VARIABILIS
FILE REFERENCE: 20629P
                                                                                                                                                                                                                                                                            FEATURE: NAME/KEY: CDS
LOCATION: (170)...(1363)
                                                                                                                                                                                                                                                                                                                                             ORGANISM: Dermacentor variabilis
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LeuSerPheLeuLeuTrp---
                                                                                  4.39e-81
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                                                                                                         Conservative: Mismatches: Indels:
                                                                                                                                                                       Length: Matches:
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-ThrLeuProGlyGlnValLeuLeuArg
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Query Match:

Percent Similarity: Best Local Similarity:

Alignment Scores: Pred. No.:

; NAME/KEY: CDS ; LOCATION: (32)...(1225) US-10-239-420-3

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SOCTWARE: pt.Fr_genes Version 1.0
SEQ ID NO 13:
LENGTH: 1693
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (88)..(1512)
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Publication No. US20030104529A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: No. US20030104529Alel Nucleic TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/10/037,270
CURRENT FILING DATE: 2002-01-04
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PRIOR TLING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
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Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
Ma, Yunging
Ren, Feiyan
Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
                                                                                SerValThrLysThrThrMetAspTyrArgValAsnValPheLeuArgGlnGlnTrpAsn 103
                                                              ATGGTCTCCGAAGTGAATATGGATTATACACTCACCATGTATTTCCAGCAGTCTTGGAAA
                                                                                                                             CCGGACTTCGGAGGGCCCCCGTCGACGTTGGGATGCGGATCGATGTCGCCAGCATAGAC
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Wang, Zhiwei
Tillinghast, John
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Zhang, Jie
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Matches:
Conservative:
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Indels:
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APPLICANT: Horrigan
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                                                                      SEQ ID NO 96
 -09-964-824A-96
                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/964,824A CURRENT FILING DATE: 2001-09-27 PRIOR APPLICATION NUMBER: US/60/236,033 PRIOR FILING DATE: 2000-09-28 PRIOR APPLICATION NUMBER: US/60/236,032 PRIOR FILING DATE: 2000-09-28 PRIOR APPLICATION NUMBER: US/60/236,028 PRIOR APPLICATION NUMBER: US/60/236,028
                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Cancer Gene Determination TITLE OF INVENTION: Sets FILE REFERENCE: 689290-73
                                                                                   PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 583
SOFTWARE: PatentIn version 3.0
                TYPE: DNA
ORGANISM: Homo sapiens
                                                    LENGTH: 1866 .
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                                                  AlaValGlnValAlaGluGlyLeuThrLeuProGlnPheIleLeuArgAspGluLysAsp
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LeuGlyIleThrThrValLeuThrMetThrThrGlnSerSerGlySerArgAlaSerLeu
                                                                                                                         CGTCTAAAGAGAAACATTGGTTACTTCATTTTGCAAACCTACATGCCTTCTACACTGATT
                                                                                                                                           HisLeuGluArgGlnMetGlyTyrTyrLeuIleGlnMetTyrIleProSerLeuLeuIle
                                                                                                                                                                                               GTGTCTAAGAAGGTGGAG----TTCACAACAGGAGCGTATCCACGACTGTCACTAAGTTTT
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                                                                                                                                                                                                                               LeuGlyCysCysThrLysHisTyrAsnThrGlyLysPheThrCysIleGluValLysPhe
                                                                                                                                                                                                                                                                                                                                           ----AGTTATGGCTATACCACTGATGACATTGAATTTTACTGGAATGGAGGAGAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                CAGAACTGCACCCTGGAGATCGAA-----
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rpThrLeuProGlyGlnValLeuLeuAr	-10-075-846-4 (1-431) x US-10-211-673-11 (1-1555)	Indels:	Fred. NO.: 9.42e // Length: 155 Score: 680.50 Matches: 161 Percent Similarity: 50.11% Conservative: 63 Best Local Similarity: 36.02% Mismatches: 150	ment Scores:	; SEQUENCE DESCRIPTION: SEQ ID NO: 11: US-10-211-673-11	: FEATURE: Coding Sequence : LOCATION: 471402 : OTHER INFORMATION:	; TOPOLOGY: linear ; MOLECULE TYPE: cDNA	TYPE: nucleic acid STRANDEDNESS: single	: INFORMATION FOR SEQ ID NO: 11: : SEQUENCE CHARACTERISTICS: : LENGTH: 1555 base bairs	TELEX: CURKNOWN TO TO NO.	TELEPHONE 732-504-1307	REFERENCE DOCKET NUMBER: T1292	REGITOTRATION NIMBER AS 2/3	FILING DATE: 29-SEP-1995	PRIOR APPLICATION NUMBER: PCT/GB95/02323	FILING DATE: 02-Aug-2002 CLASSIFICATION: <unknown></unknown>	673	OPERATING SYSTEM: Windows Version 2 Ob	COMPUTER: DISKette	COMPTITED BEADART FORM.	STATE: Nativay COMPREY: ISA	STREET: Do. Box 2000, 126 E. Lincoln Ave.	CORRESCET ADDRESS: 14	OF THE GABA-A RECEPTOR	Whiting, Paul John NVENTION: HUMAN ALPHA 4	; GENERAL INFORMATION: APPLICANT: Le Bourdelles, Beatrice	; Sequence 11, Application US/10211673 ; Publication No. US20030013158A1	RESULT 13 US-10-211-673-11	Db 983 TTCCTGGCTCTGGAGTATGCCTTTGTAAATTACATC 1021		:::	Qy 324 ProLysValSerTyrValLysAlaIleAspIleTrpMetAlaValCysLeuLeuPheVal 343	Db 863 CTAGGAATCACGACGGTGCTTACAATGACAACCATCAGCACCCACC
ОУ	Db	Qy	Дb	b B	Qy	Оу Db	Db	Qy	Db	Оу	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Оу	Db	Qy	Db	Qy	Db	Оу	Db	Qy	Db	γo	Db .	Qy	Дb
356ValSerArgGlnHisLysGluPhe,	1022 GTGGAGTACGCCTTTGCTCATTTCAACGCCGACTACAGGAAGAAGCAGAAGGCCAAGGTC 1081	348 LeuGluTyrAlaAlaIleAsnPhe 355	328 TyrValLysAlaIleAspIleTrpMetAlaValCysLeuLeuPheValPheAlaAlaLeu 347 ::: ::: ::: ::: ::: ::	ACGGTGCTGACGATGACCACGCTCATGGTCAGTGCCCGCTCCTCCCTGCCACGGGCATCA	ThrValLeuThrMetThrThrGlnSerSerGlySerArgAlaSerLeuProLysValSer	288 TrpValSerPheTrpIleAsnMetAspAlaAlaProAlaArgValGlyLeuGlyIleThr 307		268 GlnMetGlyTyrTyrLeuIleGlnMetTyrIleProSerLeuLeuIleValIleLeuSer 287	722 ATGAACTTCAAGTCCGCTGGCCAGTTCCCACGGCTCAGCCTGCACCTTCCACCTGCGGAGG 781	248 ThrLysHisTyrAsnThrGlyLysPheThrCysIleGluValLysPheHisLeuGluArg 267	662 CTGGACAAGCTGCAGCAGCTGCACCATCACCAGCTACCGCTTCACCACGGAGCTG 721	228 AlaGluGlyLeuThrLeuProGlnPheIleLeuArgAspGluLysAspLeuGlyCysCys 247	602 GGTTACTCATCGGAGGACATCGTCTACTACTGGTCGGAGAGCCAGGAGCACATCCACGGG 661	208 GlyTyrThrMetLysAspLeuValPheGluTrpLeuGluAspAlaProAlaValGlnVal 227	584 CTGGACCTGGAGAGCTAC 601	188 MetGlnLeuGluSerSerSerIleLeuCysSerProLeuProSerLeuSerLeuSerVal 207	524 TCCACTGTGGCCTGCGACATGGACCTGGCCAAATTCCCCATGGACGAGCAGGAGTGCATG 583	168 LeuIleLeuSerCysLeuMetAspLeuLysAsnPheProMetAspIleGlnThrCysThr 187	464 GAGAACAAGCTCCATCCGGCTGCAGCCCGACGGGTGATCCTGTACAGCATCCGAATCACC 523	148 AspAsnLysLeuLeuArgIlePheLysAsnGlyAsnValLeuTyrSerIleArgLeuThr 167	404 TGGCTGCCCGACACCTTCATCGTGAACGCCAAGTCGGCCTGGTTCCACGACGTGACGGTG 463	128 TrpLysProAspLeuPhePheAlaAsnGluLysGlyAlaAsnPheHisGluValThrThr 147	347 TCCTACAACCACACCAACGAGACCCTGGGCCTGGACAGCCGCTTCGTGGACAAGCTG 403	108 SerTyrArgGluTyrProAspAspSerLeuAspLeuAspProSerMetLeuAspSerIle 127	287 GCCAACATGGAGTACACCATGACGGTGTTCCTGCACCAGAGCTGGCGGGACAGCAGCAGCAGCTC 346	88 ThrThrMetAspTyrArgValAsnValPheLeuArgGlnGlnTrpAsnAspProArgLeu 107	227 GCCCCCCCCTGAATGTGGCCCTTGCCCTGGAGGTGGCCAGCATCGACCACATCTCAGAG 286	68 GlyProProValAsnValThrCysAsnIlePheIleAsnSerPheSerSerValThrLys 87		48 LeuAspLysLeuMetGlyArgThrSerGlyTyrAspAlaArgIleArgProAsnPheLys 67		35 GlyThrLysGlySerGlnProMetSer	48 TGGACGCG-CCCGCCCGGCTGCTGGCCCCGCTCCTGCTCCTCTGCGCGCAGCAGCTCCGC 106

Pred. No.: 1.26e-75 Conservative: 570.00 Parcent Similarity: 64.24% Conservative: 73 Best Local Similarity: 41.14% Mismatches: 91 Query Match: 29.75% Indels: 29 US-10-075-846-4 (1-431) x US-10-239-420-13 (1-1150) Qy 46 AspPheLeuAspLysLeuMetGlyArgThrSerGlyTyrAspAlaArgIleArgPro 64	FILING DATE: 2000-03 R OF SEQ ID NOS: 13 ARE: FastSEQ for Wind NO 13 ITH: 1150 DNA NISM: Dermacentor var 9-420-13		Qy 364IleArgLeuArgArgGlnArgArgGlnArgLeu 375 1142 TCTGCCTGCCGGCGTCACGCAGGAGCTGGCCATCCTCCGCCGGCAGGCGCCGCGGCCGCGGC- 1200 Qy 376 GluGluAspIleIleGlnGluSerArgPheTyrPheArgGlyTyrGlyLeuGlyHisCys 395
US-10-239-420-4 US-10-239-420-4 Sequence 4, Application US/10239420 Publication No. US20030096984A1 GENERAL INFORMATION: APPLICANT: Cully, Doris F. APPLICANTON: UNA MOLECULES ENCODING LIGAND GATED ION TITLE OF INVENTION: CHANNELS FROM DERMACENTOR VARIABILIS FILE REFERENCE: 2062-99-23 CURRENT FILING DATE: 2002-09-23 PRIOR APPLICATION NUMBER: 60/193,935 PRIOR APPLICATION NUMBER: 60/193,935 PRIOR PILING DATE: 2000-03-31 NUMBER OF SEQ ID NOS: 13 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 4 LENGTH: 2194 TYPE: DNA ORGANISM: Dermacentor variabilis FEATURE: RAMELKEY: CDS LOCATION: (47)(1315) US-10-239-420-4 Alignment Scores: 3.16e-73 Length: 2194 Percent Similarity: 52.53% Conservative: 91	Db 803 CTGGGCTAACCACGCTGCTCACCATCTCATCCAAGGGTATCCAAGGGAAACCTG 862 Qy 324 ProLysValSerTyrValLysAlaIleAspIleTrpMetAlaValCysLeuLeuPheVal 343	Qy 204 SerLeuSerValGlyTyrThrMetLysAspLeuValPheGluTrpLeuGluAspAlaPro 223	Db 371 TATGTGACTGTACCTAACGTCCTCGTTAGGATCAACCCGACTGGAATAATCTTGTACATG 430 Qy

ne 355 :: AC 1072	6 MetAlaValCysLeuLeuPheValPheAlaAlaLeuLeuGluTyrAlaAlaIleAsnPh	Qy 33 рь 101
G 1012	AGCTCCGACCACC	95
გ 33	erGlySerArgAlaSerLeuProLysValSerTyrValLysAlaIleAspIleT	у 31
ln 315 :: :AG 952	6 ASPALAALAPTOALAATGVALGLYLEUGLYILEThTThTVALLEUThTMTCHTHTGL 	Qy 29 Db 89
3 89	TCTTACCTGCCGTCCACACTCATCGTGGTCGTGGGTGTCCTTCTGGCTGG	83
է 29	[leProSerLeuLeuIleValIleLeuSerTrpValSerPheTrpIleAsr	27
ln 275 G 832	6 PheThrCysIleGluValLysPheHisLeuGluArgGlnMetGlyTyrTyrLeuIleGln ::::: :::: ::: 3 TACAGCTGCCTGCGCGCGCGCTCAACTTGAAGCGTTCCATTGGCCACCACCTAGTGCAG	Qy 25 Db 77
7s 255 :: :: :: ::	6 PheIleLeuArgAspGluLysAspLeuGlyCysCysThrLysHisTyrAsnThrGlyLy:	Qy 23 Db 71
31n 235 2AA 715	6 PheGluTrpLeuGluAspAlaProAlaValGlnValAlaGluGlyLeuThrLeuProGl 	Qy 21 Db 65
11 215 NG 658	6 LeuCysSerProLeuProSerLeuSerLeuSerValGlyTyrThrMetLysAspLeuVal :::::: 8AAGACGACAAAGGAGGTTGAG	Qy 19 Db 63
le 195	O H	
sp 175	6 LysAsnGlyAsnValLeuTyrSerIleArgLeuThrLeuIleLeuSerCysLeuMetAsp ::::: :::	Qу ¹⁵
te 155 :: AC 520	6 AsnGluLysGlyAlaAsnPheHisGluValThrThrAspAsnLysLeuLeuArgIlePhe	Qy 13 Db 46
.a 135 C 460	7 LeuAspLeuAspProSerMetLeuAspSerIleTrpLysProAspLeuPhePheAla ::::: :::	Qy 11 Db 40
er 116 1 2C 400	7 PheLeuArgGlnGlnTrpAsnAspProArgLeuSerTyrArgGluTyrProAspAspSe: 	Qy 97 Db 344
11 96 :: :G 343	ii aī	Qy 7 Db 28
sn 76 AG 283	TyrAspAlaArgIleArgProAsnPheLysGlyProProValAsnValThrCysA	Qy 58 Db 224
1y 57 GC 223	GlySerGlnProMetSerProSerAspPheLeuAspLysLeuMetGlyArgThrSerG 	Oy 38 Db 174
ys 37 :: :AG 173	ProGlyGlnValLeuLeuArgValAlaLeuAlaLysGluGluValLysSerGlyThYL :: :: CCTGGTTCGCTCAGGCTGTCGACCACATCGACAAAGGATACCCAGCACC	Qy 18 Db 123
	6-4 (1-431) x US-10-239-420-4 (1-2194)	US-10-075-84
	imilarity: 33.33% Mismatches: 133 29.09% Indels: 94 9 Gaps: 14	Best Local S Query Match: DB:

Search completed: July 1, 2003, 01:01:34 Job time: 248.481 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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Command line parameters:

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-DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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 16154066 seqs, 8097743376 residues
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	0 0 '	Result
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rs	AKULE/68 MUS muscu BQQ44592 UI - M-EHO- BI736340 603360049 BI825190 603372067 BB653397 BB653397 BB653397 BB653397 BB653392 603290479 BQ067922 AGENCOURT BM547796 AGENCOURT AW077068 fj04d06. y BI757807 603183256 BM964113 UI - M-EQO- BI913857 603183256 BQ067799 AGENCOURT AW280976 fj48d02. y BI829118 603079231 BI552703 603193953 BG189196 RST8236 A BH1824761 603033645 BI681394 460778 M BM129587 ff20e03 ABM129587 ff20e03 ABM1295	AU16 AV7 AV7 AU17 AU17 AU17 AU17 AU17 AU17 AU17 AU1	:

EI AA AA AA AA BA BAREFERENCE 1	ORGANISM O	SOURCE J	KEYWORDS E	VERSION A	ACCESSION A	DEFINITION A	LOCUS A	AU169868	RESULT 1
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryziinae; Oryzias. 1 (bases 1 to 662)	Oryzias latipes	Japanese medaka.	EST.	AU169868.1 GI:12591937	sequence. AU169868	AU169868 Ol-br-ad cDNA Oryzias latipes cDNA clone br5332, mRNA	AU169868 662 bp mRNA linear EST 29-JAN-2001		

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2001)
Contact: Mita K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mita, K., Ishikawa, Y. and Yamauchi, M. Establishment of cDNA database of medaka,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Research Group
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/sex="female/male mixed"
/tissue_type="brain"
/dev_stage="adult"
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/strain="HNI"
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
This consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; V
Mammalia; Eutheria; Rodentia; Sciurognath
1 (bases 1 to 779)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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UI-M-EWO-bxh-j-02-0-UI.rl NIH_BMAP_EWO
IMAGE:5708257 5', mRNA sequence.
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/tissue_type="whole brain"
/dev_stage="embryo 15.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/lab_host="DH10B (T1 phage resistant)"
/note="organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
/note="organ: brain; Vector: pX-Asc; Site_1: EcoR I;
/note="or
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                                                                                                                                                                                                                                                                                               (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Head (NIMH), Hemin Chin, Ph.D., program coordinator." 167 c 165 g 225 t
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/strain="C57BL/6"
/db_xref="taxon:10090"
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/clone_lib="NIH_BMAP_EWO"
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US-10-075-846-4 (1-431)

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Homo sapiens CDNA HTC clones (hopublished (2000) Contact: Zeguang Han Chinese National Human Genome 351 Guo Shoujing Road, Zhangji 201203, P. R. China Tel: 86-21-50801919 (ex.45) Fax: 86-21-50801922
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Eukaryota; Metazoa; Chordata; Craniata; Hominidae;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 678)
1 (bases 1 to 678)
                                                                        Gu,Y., Peng,Y., Song,H., Huang,Q.,
Li,N., Qian,B., Liu,F., Qu,J., Gao,
,S., Gu,W., Tu,Y., Jia,J., Fu,G., F
Chen,J., Chen,Z. and Han,Z.
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                            Genome Center at Shanghai Zhangjiang Hi-Tech Park,
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                                                                                  Yang,Y., Gao,G., Xiao,H., Xu,X,X., Cheng,Z., Xu,Z., Zeng,L.,Ren,S., Zhong,M., Lu,G., Hu,R.,
                             Pudong,
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This clone is available
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                   euGlyCysCysThrLysHisTyrAsnThrGly
                                       GTGCAAGTTGCTGAAAGATTGACCCTTGCCCAAGGTTATTTTGAAAGAAGAAGACGACGGACC
                                              ValGlnValAlaGluGlyLeuThr-LeuProGlnPheIleLeuArgAspGlu-LysAspL
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/db_xref="taxon:9606"
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41	29 LysGluGluValLysSerGlyThrLysGlySerGln	9 LeuSerPheLeuLeuTrpThrLeuProGlyGlnValLeuLeuArgValAlaLeuAla 28 ::: :::	37.90% Indels: 11 Gaps:) x BC027094 (1-2991)	4.05e-97 853.50 64.10% 48.21%	877 a 587 c 607 g 920 t	<pre>/tissue_type="Eye, retina, mouse strain C57Bl\6" /clone_lib="NIH_MGC_94" /lab_host="DH10B" /note="Vector: DCMY-SPORT6"</pre>		This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 14149638 This clone has the following problem: frame shifted. Location/Qualifiers	tributior he I.M.A. RAK Plate	Contact: amg@bcm tmc.edu Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.	DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/	Email: ggapbs-r@mail.nih.gov Tissue Procurement: The Cepko Laboratory .cDNA Library Preparation: Life Technologies, InccDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	C Project URL: http://mgc.nci.nih.gov t: MGC help desk	Strausberg,R. Direct Submission Submitted (04-APR-2002) National Institutes of Health, Mammalian Submitted (04-APR-2002) Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute 31 Center Drive Poom 11003 Betheada ND 20802-2500	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 2991)	BC027094 BC027094.1 GI:20072562 HTC. house mouse.	BC027094 2991 bp mRNA linear HTC 07-AUG-2002 Mus musculus, glycine receptor, beta subunit, clone IMAGE:5360070, mRNA.	
RESULT 5 BC022502 LOCUS		Оy	Qу	Qу	Qy Db	Qу	Qy	Оу	Qу	Qy	ОУ	Qy Db	dd	Qy Db	Qy .	Оу .	Qy	Db
BC022502 2593 bp mRNA linear HTC 04-FEB-2002	362 GluPheIleArgLeuArgArgArgGInArg 371	46 AlaLeuLeuGluTyrAlaAlaIle ::: ::: 54 TCCCTCGTGGAGTACGCTGTGCTCCAGGTG	326 ValSerTyrValLysAlaIleAspIleTrpMetAlaValCysLeuLeuPheValPheAla 345	306 IleThrThrValLeuThrMetThrThrGlnSerSerGlySerArgAlaSerLeuProLys 325 ::: ::::: ::::	286 LeuSerTrpValSerPheTrpIleAsnMetAspAlaAlaProAlaArgValGlyLeuGly 305	266 GluargGlnMetGlyTyrTyrLeuIleGlnMetTyrIleProSerLeuLeuIleVallle 285	247 CysThrLysHisTyrAsnThrGlyLysPheThrCysIleGluValLysPheHisLeu 265	228 AlaGluGlyLeuThrLeuProGlnPheIleLeuArgAspGluLysAspLeuGlyCys 246 :: :::::::: :: 797GAAAAAATTGCTTTACCTCAATTTGATATTAAAAAGGAGGATATCGAATATGGCAAC 853	208 GlyTyrThrMetLysAspLeuValPheGluTrpLeuGluAspAlaProAlaValGlnVal 227	188 MetGlnLeuGluSerSerSerIleLeuCysSerProLeuProSerLeuSerLeuSerLeuSerVal 207	168 LeuIleLeuSerCysLeuMetAspLeuLysAsnPheProMetAspIleGlnThrCysThr 187 ::: :::	148 AspAsnLysLeuLeuArgIlePheLysAsnGlyAsnValLeuTyrSerIleArgLeuThr 167 :::	120 11 PLYSE COAS PEGET RETIREMENTS LILYSG LYALDASHETHERS LIVELTITE 147	SerTyrArgGluTyrProAspAspSerLeuAspLeuAspProSerMetLeuAspSerIle ::: ::: ::: GACTTCAGAGGCTCAGATGCACTGACAGTTGACCCCACCATGTATAAGTGCTTG GACTTCAGAGGCTCAGATGCACTGACAGTTGACCCCACCATGTATAAGTGCTTTG GACTTCAGA	92 TyrArgValAsnValPheLeuArgGlnGlnTrpAsnAspProArgLeu	72 ASNVALTHICYSASNILePheIleASnSerPheSerSerValThrLySThrThrMctAsp 91 :::	52 MetGlyArgThrSerGlyTyrAspAlaArgIleArgProAsnPheLysGlyProProVal 71 :::	258 CACCCGAGGACCTGGCCCGTGTGCCCCCCAAC-TCCACCAGCAATATCTTGAACAGGCTG 316

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CAGCAGTCAGCAGAGGACCTTGCCCGAGTACCTGCCAACTCCAACTTCCAACTCCAACTTGACC LyśLeuMetGlyArgThrSerGlyTyrAspAlaArg11eArgProAsnPheLysGlyPro ::: ::: AGGTTATTGGTCAGTTATGATCCCAGGATAAGACCAAACTTCAAAGGCATT	AlaLysGluGluValLysSerGlyThrLysGlySerGlnProMet	≥= = .	36.97% Indels: 11 Gaps:	Scores: 1.54e-94 Length: 2593 milarity: 63.78% Conservative: 64 Similarity: 47.45% Mismatches: 89	824 a	/tissue_type="Brain, hypothalamus" /clone_llb="NIH_MGC_96" /lab_host="DH10B"	/or /db /db	passed the following selection criteria: matched mRNA gi: « This clone has the following problem: frame shifted. Location/Qualifiers 1. 2593	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 32 Row: b Column: 19 This clone was salected for full length sequencing because it	Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www.shgc.stanford.edu	Email: cgapbs remail.nih.gov Email: cgapbs remail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshivuki and Plero Carninci (RIKEN)	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk	Strausberg, R. Strausberg, R. Direct Submission Submitted (01-FBB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer	T 0) H	Homo sapiens, glycine receptor, beta, clone IMAGE:4792516, mRNA. BC022502 BC022502.1 GI:18490294 HTC. HTC. HTC.
RESULT 6 BE981841 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	Qy	D Qy	Qy Db	Qy ,	Qy Db	Qy Db	Qy	. Qy . Db	Qy Db	Qy	Qy Db	Qy	Оy	Qy Db	Qy .	Qy Db
BE981841 N UI-M-CGOp-bdd-h-07-0-UI.S1 NIH.BMAP_Ret4_S2 Mus musculus cDNA clone UI-M-CGOp-bdd-h-07-0-UI 3', mRNA sequence. BE981841.1 GI:10651376 EST.	360 HisLysGluPheIleArgLeuArgArgArgGlnArg 371 :: :::::: 1180 GAAGCTGAAAAAGCCAGAATTGCTAAGGCTGAGCAA 1215	344 PheAlaAlaLeuLeuGluTyrAlaAlaIleAsnPheValSerArgGln 359 ::: ::: :::	324 ProLysValSerTyrValLysAlaIleAspIleTrpMetAlaValCysLeuLeuPheVal 343 	304 LeuGlyILeThrThrValLeuThrMetThrThrGlnSerSerGlySerArgAlaSerLeu 323 	284 ValIleLeuSerTrpValSerPheTrpIleAsnMetAspAlaAlaProAlaArgValGly 303	264 HisLeuGluArgGlnMetGlyTyrTyrLeuIleGlnMetTyrTleProSerLeuLeuIle 283	245 GlyCysCysThrLysHisTyrAsnThrGlyLysPheThrCysIleGluValLysPhe 263	226 GlnValAlaGluGlyLeuThrLeuProGlnPheIleLeuArgAspGluLysAspLeu 244 ::: ::: ::::::::	206 ServalGlyTyrThrMetLysAspLeuvalPheGluTrpLeuGluAspAlaProAlaval 225	186 CysThrMetGlnLeuGluSerSerSerIleLeuCysSerProLeuProSerLeuSerLeu 205 	166 LeuThrLeuIleLeuSerCysLeuMetAspLeuLysAsnPheProMetAspIleGlnThr 185	146 ThrThrAspAsnLysLeuLeuArgIlePheLysAsnGlyAsnValLeuTyrSerIleArg 165	126 SerileTrpLysProAspLeuPhePheAlaAsnGluLysGlyAlaAsnPheHisGluVal 145 :::	108SerTyrArgGluTyrProAspAspSerLeuAspLeuAspProSerMetLeuAsp 125 :::	90 MetAspTyrargValAsnValPheLeuargGlnGlnTrpAsnAspProArgLeu 107 	70 ProvalasnvalThrCysAsnIlePheIleAsnSerPheSerSerValThrLysThrThr 89 ::: 335 CCTGTTGATGTAGTCAACACATTTTAATTAACAGTTTTGGATCCATTCAAGAAACAACA 394

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Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements The tissue for this library was contributed by Dr. Xin-Yuan Fu, Yale University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda,
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
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    eLysGlyProProValAsnValThrCysAsnIlePheIleAsnSerPheSerSerValTh
                                                                        TTTTCTGGACAAACTAATGGGGAGGACATCGGGGTATGATGCAAGAATCAGACCCAACTT
                                                                                                                                                                                                   aLeuAlaLysGluGluValLysSerGlyThrLysGlySerGlnProMetSerProSerAs 46
                                                                                                                                                                                                                                                ACACTTTCGGACACTAGTTTCTGGATTTTACTTCTGGGAAGCCGCACTGTTACTGAGTTT
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                                                                                            pPheLeuAspLysLeuMetG1yArgThrSerG1yTyrAspA1aArg11eArgProAsnPh
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_Ret4_S2 library is a subtracted library, ultimately derived from mouse retina tissue libraries at various stages of development. For a detailed description of the library from which this clone was derived, please visit our web site at brainest.eng.uiowa.edu. The tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAG_SEQ=None found"
159 c 144 g
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University School of Medicine
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/db_xref="taxon:10090"
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Contact: Chin, H
National Institute of Mental Health
National Institute Blvd. Room 7N-7190, MSC
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                                                                                                                                                                                               Email: mEST@mail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
clones from RESEARCH GENETICS. It should be noted that Bento Soares
is generating a small number of additional specialized
non-redundant arrays of BMAP cDNAs whose availability will be
considered under appropriate and limited collaborative arrangements
The tissue for this library was contributed by Dr. Xin-Yuan Fu,
Yale University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 301 443 1706
Fax: 301 443 9890
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/organism="Mus musculus"
/strain="c57BL/6J"
/db_xref="taxon:1090"
/clone="UI-M-GS0p-bdc-d-08-0-UI"
/clone_lib="NIH_BMAP_Ret4_S2"
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43SerProSerAspPheLeuAsp [1]::: [1]::: [1]::: [24 CAGCAGTCAGCAGAGGACCTTGCCCGAGTACCTGCCAACTCCACTACATATCTTGAAC [50 LysLeuMetGlyArgThrSerGlyTyrAspAlaArgIleArgProAsnPheLysGlyPro [51]::: [1]::: [1] [1]	AlaLysGluGluValLysSerGlyThrLysGlySerGlnProMet	ThrLeuSerPheLeuLeuLeuTrp	36.97% Index:	Alignment Scores: 1.54e-94 Length: 2593 Score: 832.50 Matches: 186 Score: 53.78% Conservative: 64 Best Local Similarity: 47.45% Mismarches: 89 Best Local Similarity: 47.45% Mismarches: 89	824 a	/tissue_type="Brain, hypothalamus" /tissue_type="Brain, hypothalamus" /clone_lib="NHIH_MGC_96" /lab_host="DHIOB" /pote="Vector: DHIOBSCTint"		passed the following selection criteria: matched mRNA gi: 4504022 This clone has the following problem: frame shifted. Location/Qualifiers 1 2503	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 32 Row: b Column: 19	Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (Linl) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www-shog.stanford.edu	Email: cgapbs-remail.nih.gov Email: cgapbs-remail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshivuki and Diero Carninci (DTKEN)	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov		Homo saptens. Homo saptens Homo saptens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
RESULT 6 BE981841 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	Qу	Oy	Фу	Qy	. Qy Db	Оy	Qy Db	Qу	ДУ	Qу	. pb	Qу	ОУ Db	Qy Db	Db Oy	Qy
BE981841 692 bp mRNA linear EST 29-APR-2002 N UI-M-CCOp-bdd-h-07-0-UI.S1 NIH_BMAP_Ret4_S2 Mus musculus cDNA clone UI-M-CGOp-bdd-h-07-0-UI 3', mRNA sequence. 4 BE981841 BE981841.1 GI:10651376 EST.	360 HisLysGluPheIleArgLeuArgArgArgGlnArg 371	344 PheAlaAlaLeuLeuGluTyrAlaAlaIleAsnPheValSerArgGln 359	324 ProLysvalSerTyrValLysAlaIleAspileTrpMetAlaValCysLeuLeuPheVal 343	304 LeuGlyIleThrThrValLeuThrMetThrThrGlnSerSerGlySerArgAlaSerLeu 323 1000 CTGGGTATCTTCTCAGTCCTCAGCCTTGGCCTCTGAGTGCACAACCCTTGCCGCTGAGCTT 1059	284 ValileLeuSerTrpValSerPheTrpIleAsnMetAspAlaAlaProAlaArgValGly 303	264 HisLeuGluArgGlnMetGlyTyrTyrLeuIleGlnMetTyrIleProSerLeuLeuIle 283	245 GlyCysCysThrLysHisTyrAsnThrGlyLysPheThrCysIleGluValLysPhe 263	226 GlnValAlaGluGlyLeuThrLeuProGlnPheIleLeuArgAspGluLysAspLeu 244 ::: :::	206 SerValGlyTyrThrMetLysAspLeuValPheGluTrpLeuGluAspAlaProAlaVal 225	186 CysThrMetGlnLeuGluSerSerSerIleLeuCysSerProLeuProSerLeuSerLeu 205	166 LeuThrLeuIleLeuSerCysLeuMetAspLeuLysAsnPheProMetAspIleGlnThr 185	146 ThrThrAspAsnLysLeuLeuArgIlePheLysAsnGlyAsnValLeuTyrSerIleArg 165	126 SerTleTrpLysProAspLeuPhePheAlaAsnGluLysGlyAlaAsnPheHisGluVal 145 :::	SerTyrArgGluTyrProAspAspSerLeuAspLeuAspProSerMetLeuAsp ::: ::: ::: ::: CCCAGTGATTTTAGGGGTTCAGATGCACTGACAGTGGATCCAACAATGTACAAG	90 MetAspTyrArgValAsnValPheLeuArgGlnGlnTrpAsnAspProArgLeu 107 	70 ProvalasnvalThrCysasnIlePheIleAsnSerPheSerServalThrLysThrThr 89 ::: :: 335 CCTGTTGATGTAGTCAACATTTTATTAACAGTTTTGGATCCATTCAAGAAACAACA 394

A.08e-90 Length: 692 Score: 789.50 Matches: 157 Percent Similarity: 78.95% Conservative: 8 Best Local Similarity: 75.12% Mismatches: 28 Ouery Match: 12 Mismatches: 28 Ouery Match: 169 Oy	Seq primer: M13 Forward POLYA=NO. Location/Qualifiers 1. 692 /organism="Mus musculus" /strain="C57BL/SJ" /db_xref="taxon:10090" /clone="II-M-CGDp-bdd-h-07-0-UI" /clone="II-M-CGD-bdd-h-07-0-UI" /clone="II-M-CGD-bdd-h-07-0-UI" /clone="II-M-CGD-bdd-h-07-0-UI" /clone="II-M-CGD-bdd-h-07-0-UI" /clone="II-M-CGD-bdd-h-07-0-UI" /clone="II-M-CGD-bdd-h-07-0-UI" /clone="II-M-CGD-bdd-h-07-0-UI" /clone=	Metas Metas Metas Metas to to to to to fo fo fo fo fo fo fo fo fo fo fo fo fo
GOOL Executive Director MSC 9643, Bethesda, MD 20892-9643, USA Tel: 301 443 1706 Fax: 301 443 1706 Fax: 301 443 1890 Email: mEST@mail.nih.gov Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements The tissue for this library was contributed by Dr. Xin-Yuan Fu, Yale University School of Medicine Seq primer: M13 Forward POLYA=NO. Location/Qualifiers	Oy 206 rvalGlyTyThrmetLysAspLeu 214 Db 668 CTTTGGGTACACAATGAATCTC 692 RESULT 7 BE981459 BE981459 PE981459 BE981459 PEPR-2002 PEPRINTION UI-M-CGOp-bdc-d-08-0-UI-S1 NIH_BMAP_Ret4_S2 Mus musculus cDNA clone ACCESSION BE981459 ACCESSION BE981459 PEPR-2002 PEPR-2002 VERSION BE981459 PEPR-2003 PEPR-2003 PEPR-2003 PEPR-2003 SOURCE Douse mouse PEPR-2004 PEPR-2004 PEPR-2005 PEPR-2	290 CAAAGGTCCTCCAGTTAATGTCACAT 86 rLysThrThrMetAspTyrArgValA :::

Score: Pred

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Percent Similarity:
Best Local Similarity:
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US-10-075-846-4 (1-431) x BG404477 (1-817)
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: The Cepko Laboratory
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//db_xref="taxon:10090"
//clone="IMAGE:4527768"
//clone_lib="NIH_MGC_94"
//tissue_type="retina"
//tissue_type="r
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AGENCOURT_8930535 NIH_MGC_94
5', mRNA Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
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National Institutes of Health, Mammalian
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                                                                                                            /organism="Mus musculus"
/db_xref="taxon:10090"
/db_xref="Taxon:10090"
/clone=_1ib="NMAGE.646531"
/clone__1ib="NH_MGC_94"
/tlssue_type="retina"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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 receptor,
AK013727
AK013727.1
HTC; CAP t
                                       AK013727 2475 bp mRNA linear HTC 19. Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone:2900059A15:gamma-aminobutyric acid receptor, subunit alpha 4, full insert sequence.
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                                                                                                                                             GCCCCAAATAGCTAAGGCTGGACCAA
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                                                                                                                                                                                                                                                         AAAGCGCTGGATGTGTGGCTCATTGCCTGCCTGCTCTTCGGGTTTGCCCTCCCCCTCGTGG
                                                                                                                                                                                                                                                                                                                SerPheTrpIleAsnMetAspAlaAlaProAlaArgValGlyLeuGlyIleThrThrVal
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S Adachi,J., Alzawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Adachi,J., Alzawa,K., Bono,H., Brownstein,M., Bult,C., Arakawa,T., Baldasrelli,R., Bono,H., Furuno,M., Hanagaki,T., Carninct,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hirawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Myyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Ohido,T., Owa,C., Quackenbush,J., Salto,H., Salto,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Sahto,H., Salto,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Sognbe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamanura,T., Yamanaka,I., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
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URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222
Fax:81-45-503-9216)
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7 AlaThrLeuSerPheLeuLeuLeuTrpThrLeuProGlyGlnValLeuLeuArgValAla 26
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SSLVOVDLIGOTVSSETIKSITGEYIVMTVYFHLRRKKGYFMJOTYIPCIMTVILSQV
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WIDKELKYDGPIEILELNNMMYTKVWTPDTFFRNGKKSVSHNMTAPNKLFRIMNGTI
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GluSerArgPheTyrPheArgGlyTyrGlyLeuGlyHisCysLeuGlnAlaArgAspGly
                                                                  GluPheIleArgLeuArgArgArgGlnArgArgGlnArgLeuGluGluAspIleIleGln
                                                                                                           TTTGTATTTCGGCTCTTATTGAGTTTGCTGCTGTCAACTAT-----
                                                                                                                                          PheValPheAlaAlaLeuLeuGluTyrAlaAlaIleAsnPheValSerArgGlnHisLys
                                                                                                                                                                               TCTTTGCCCAAAGTGTCCTATGCGACTGCCATGGATTGGTTCATAGCTGTCTTTTTGCT
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                                                                                                                                                                                                                                                                                                                                                                           /note="organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and Eco closed into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: http://fc.incom/spices.com/uRL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="CSODF029YP18"
/clone=lib="LTI_FL013_FBrn1"
/dev_stage="pooled tissue from week, 24 week and 26 week)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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IMAGE:5685752 5', mRNA sequence.
BQ042344
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: MGC clone distribution information can be
                                                                                                                    Mammalia; Eutheria; Rodentia; Sciurognati
1 (bases 1 to 802)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                       BQ042344.1
                                                                                                            Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                           house mouse.
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Mus musculus
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http://image.llnl.gov
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|AGACCAAACTTCAAAGGCATTCCTGTTGATGTAGTAGTCAACATTTTTATTAATAGTTTT
           GlyAlaAsnPheHisGluValThrThrAspAsnLysLeuLeuArgIlePheLysAsnGly
                                                                                                                                                                                         GGATCCATTCAAGAGACAACAATGGACTATAGAGTTAACATTTTCTTGAGACAGAAATGG
                                                                                          LeuAspProSerMetLeuAspSerIleTrpLysProAspLeuPhePheAlaAsnGluLys
                                                                                                                                             AsnAspProArgLeu------SerTyrArgGluTyrProAspAspSerLeuAsp
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                                                             GTTGACCCCACCATGTATAAGTGCTTGTGGAAACCTGACTTATTCTTTGCAAATGAAAAA
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/strain="C57BL/6"
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                                                                                                                                                                                                                                                    .S., Masuho,Y., Isogai,T.)
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 29
Tel: 81-438-52-3975
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,S., Masuh
                                                                                                                                                                  Email: genomics@hri.co.jp
HRI human cDNA project, 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 817)
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                                                                                                                                                                                                                                                                                                                                     human cDNA project (Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y., to,K., Yamamoto,J., Nishikawa,T., Nakamura,Y., Nagai,T., Sugano, Masuh,Y., Isogai,T.)
                     207
                                                                                                                                                                                                                                                                                                                                                                                                          Sugiyama, T., Ishii, S.,
               /note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction" a 207 c 198 g 202 t 3 others
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                                                                                      /db_xref="taxon:9606"
/clone="NT2RP4001569"
/clone_lib="NT2RP4"
                                                           /cell_type="teratocarcinoma"
/cell_line="NT2"
                                                                                                                              /organism="Homo sapiens"
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Nagai,T., Sugano,S., Mas
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1942 bp mRNA linear HTC. Homo sapiens, gamma-aminobutyric acid (GABA) A receptor, clone IMAGE:5178575, mRNA.
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                                                                                                                                                                                                          TCCATCGTGGAGCACCGT---CTGGTCTCGAGGAATGTTGTCTTCGCCACAGGTGCCTAT
                                                                                                                                                                                                                                                                                                                                                                             TACTGGCGAGGCGGGACAAGGCTGTTACCGGAGTGGAAAGGATTGAGCTCCCGCAGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
Tissue Proparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (06-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.hgsc.bcm.tmc.edu/cdna/Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hüly
Yoon, V.S., Kowis, C.R., Lawrence, S., Mart
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/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:5178575"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="LocusID:2567"
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Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 948)
                                                                                                                                              AL539373 LTI_FL013_FBrn1
                                                                                                              prime, mRNA sequence
AL539373
                                                                   human.
                                                                                                 AL539373.1
                                                                                                                                                                                                                                                                                                                                                                                                                      AlaAlaLeuLeuGluTyrAlaAlaIleAsnPheValSerArgGlnHisLys 361
                                                                                                                                                                                                                                                                                                              GlyIleThrThrValLeuThrMetThrThrGlnSerSerGlySerArgAlaSerLeuPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CysThrLysHisTyrAsnThr-----GlyLysPheThrCysIleGluValLysPheHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValAlaGluGlyLeuThrLeuProGlnPheIleLeuArgAspGluLysAspLeuGlyCys ::: ||| |||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ValGlyTyrThrMetLysAspLeuValPheGluTrpLeuGluAspAlaProAlaValGln
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                                                                                                                                                                                                                                                                                           CGCGTGTCCTACGTGACCGCCATGGACCTTTTTGTGACTGTGCTTCCTGTTTTGTCTTC
                                                                                                                                                                                                                                                                                                                                                           GGCATCACCACGGTGCTGACCATGACCACCCTGAGCACCATCGCCAGGAAGTCCTTGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuGluArgGlnMetGlyTyrTyrLeuIleGlnMetTyrIleProSerLeuLeuIleVal 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCACAGAAATCGTGACAACGTCTGCAGGTGATTATGTTGTCATGACTATATTTTTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACCAGAAATCATGGCGGCTTTATCAGTTT-----GACTTCATGGGCCTCAGAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATGGCTATCCCAAAGAAGAAATGATTTATAGATGGAGAAAAAATTCAGTGGAGGCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ThrMetGlnLeuGluSerSerSerIleLeuCysSerProLeuProSerLeuSerLeuSer
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                                                                                                 GI:12868529
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o sapiens cDNA clone CSODF033YM17 5
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Genoscope
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IleArgLeuThrLeuIleLeuSerCysLeuMetAspLeuLysAsnPheProMetAspIle 183
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                                                                                                                                                                                                                                                                                                                                                           SerValThrLysThrThrMetAspTyrArgValAsnValPheLeuArgGlnGlnTrpAsn 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProAsnPheLysGlyProProValAsnValThrCysAsnIlePheIleAsnSerPheSer
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                                                                 GGGGTCACAGTGAAAAAATCGAATGATTCGACTGCATCCTGATGGAACAGTTCTCTATGGA
                                                                                                       GluValThrThrAspAsnLysLeuLeuArgIlePheLysAsnGlyAsnValLeuTyrSer 163
                                                                                                                                                       GCTGACCAACTCTGGGTACCAGACACCTACTTTCTGAATGACAAGAAATCATTTGTGCAT
                                                                                                                                                                                               LeuAspSerIleTrpLysProAspLeuPhePheAlaAsnGluLysGlyAlaAsnPheHis 143
                                                                                                                                                                                                                                          GACAAAAGGCTTTCTTATTCTGGAATCCCA----CTGAACCTCACCCTAGACAATAGGGTA 410
                                                                                                                                                                                                                                                                   AspProArgLeuSerTyrArgGluTyrProAspAspSerLeuAspLeuAspProSerMet
                                                                                                                                                                                                                                                                                                                                ATGGTCTCCGAAGTGAATATGGATTATACACTCACCATGTATTTCCAGCAGTCTTGGAAA 353
                                                                                                                                                                                                                                                                                                                                                                                                                      CCGGACTTCGGAGGGCCCCCCCTCGACGTTGGGATGCGGATCGATGTCGCCAGCATAGAC
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/clone_llb="LTI_FLO13_FBrn1"
/clone_llb="LTI_FLO13_FBrn1"
/dev_stage="pooled tissue from post conception fetuses (20
/dev_stage="pooled tissue from post conception for fix strand
/note="Porlan fetuse"/
/note="Porlan fetuse from post conception for fix prime
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the NotI and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
u==vuland 20850, USA Fax : (1) 301 610 8371 Email :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Location/Qualifiers
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Фр	ОУ	Дy	Фy	Фb	ОУ	ДУ	Дb
304 906	284 846	264 786	244 729	224 669	204 615	184 591	531
LeuGlyIleThrThrValLeuThrMetThrThrGlnSerSer 317	VallleLeuSerTrpValSerPheTrpIleAsnMetAspAlaAlaProAlaArgValGly 303 	HisLeuGluArgGlnMetGlyTyrTyrLeuIleGlnMetTyrIleProSerLeuLeuIle 283 ::: ::: ::::	LeuGlyCysCysThrLysHisTyrAsnThrGlyLysPheThrCysIleGluValLysPhe 263 :::	AlaValGlnValAlaGluGlyLeuThrLeuProGlnPheIleLeuArgAspGluLysAsp 243	204 SerLeuSerValGlyTyrThrMetLysAspLeuValPheGluTrpLeuGluAspAlaPro 223	GlnThrCysThrMetGlnLeuGluSerSerSerIleLeuCysSerProLeuProSerLeu 203	531 CTCCGAATCACAACCACAGCTGCATGTATGATGGATCTTCGAAGATATCCACTGGATGAG 590

Search completed: July 1, 2003, 00:55:27 Job time: 2277.88 secs

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-MODEL-frame+_p2n.model -DEV-xlp
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-DB--GenEmbl -QFMT-fastap -SUFFIX-p2n.rge -MIMMATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-bits -START-1 -END--1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST-45
-DCCALIGN-200 -THR_SCORE-pct -THR_MXX-100 -FIR_MIN-0 -ALIGN-15 -MODE-LOCAL
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-FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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31: em_htg_inv:*
32: em_htg_other:*
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37: em_htg_wart:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_hum:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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RESULT 1

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RESULT 2
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                                                                                                                                                                                                                  Submitted (07-APR-1997) Sanger Centre, Hinxton, Cambridgeshire, CB10 1RQ, UK. E-mail enquires: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk information in the requests: clonerequest@sanger.ac.uk information in the sequence is the entire insert of clone U35G3. This sequence has been finished according to sequence map criteria as sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
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Sequence 6 from Patent WO0058461.
AX037570
                                                                                                                               The true left end of clone U35G3 is at 1 in this sequence. right end of clone U35G3 is at 39796. U35G3 is from the Lawrence Livermore National Laboratory flow-sorted X chromosome cosmid library LLOXNCO1.
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/db_xref="taxon:9606"
9337 c 9355 g 1047
     /clone="LL0xNC01-35G3"
/clone_lib="LL0xNC01"
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/db_xref="taxon:9606"
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                   /note="L1MB8 31110. .3140
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/note="MER5A repeat: matches 7.
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                                                    30830.
                                                                    /note="AluSg repeat:
incomplete repeat"
30706. .30781
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/note="MIR
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incomplete repeat"
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/note="AluSx repeat: matches 44.
incomplete repeat"
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incomplete repeat"
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27270. .27486
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14745. .14874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          te="MLT1A1 repeat: matches 365.
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te="L1PA6 repeat: matches 571. .457 of consensus"
              ылмы repeat: matches 413.
.31403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AluJb repeat: matches 295. .1 of .20454
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                                                                                                                                                                                                                                            AUTHORS
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                                                                                                        Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
                                                                                                                                                              Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Calmoppiano, A., Castle, A., Choepel, Y., Colangelo, W., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Cra
Mammalla; Eutherla; Primates; Cat
1 (bases 1 to 170676)
Birren, B., Linton, L., Nusbaum, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          170676 bp DNA linear PRI 18-AUG-
Homo sapiens chromosome 8, clone RP11-67N21, complete sequence.
AC026258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 SerSerIleLeuCysSerProLeuProSerLeuSerLeuSerVal 16
                                  Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
                                                                                                                                                 Dodge, S., Domino, M.,
                                                                                                                                                                                                                                        Birren, B., Linton, L.,
                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                             Homo sapiens chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                           AC026258.4 GI:14579802
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/note="AluSg repeat:
incomplete repeat"
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37468. .38250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34108. .34350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=-"MIR repeat: matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note-"MIR repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MIR repeat: matches 247. .6 of consensus"
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93.33%
90.67%
9
                 Meneus,L.,
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68.00
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Mihova,T., Miranda,C., Mlenga,V., Morrow,J.
Norman,C.H., O'Connor,T., O'Donnell,P.,
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                                                                                                                                                                                                                                                                                               8, clone
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Matches:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                             and Lander, E. RP11-67N21
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Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McBwan, P., McKernan, K., McPhaeters, R., Meldrim, J., Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigillo, J., Vassilev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (18-AUG-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 1, 2001 this sequence version replaced gi:14336597. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., EitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: L7482 Center clone name: 67_N_21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center code: WIBR Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Whitehead Institute/ MIT Center for Genome
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1929. .2057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (913.
                                                                                                   /rpt.
                                                                                                                                 complement(3538
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/chromosome="8"
/rpt_family="MSTB"
                                                                                                                                                                       /rpt_family="L2"
                                                                                                                                                                                                                                            /rpt_fami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="MER58"
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                                                                                                                                                                                                                                                                                                                        rpt_family="L1MEd"
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                                                             _family="MLT1J1"
lement(302)
                                                                                                                                                                                                                                                ly-"AT_rich"
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repeat_region

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pt_fam:

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repeat_region repeat_region repeat_region repeat_region

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/rpt_family="AT_rich"
8672. .8719
                                                                                                                                                                                                                            complement(19826. .20188)
/rpt_family="THE1B"
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/rpt_family="L2" .
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/rpt_family="L2"
                                                                                                                                                                                                                                                                                                                   complement(18562. .18744)
/rpt_family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(12500.
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complement(10813. .10901)
   /rpt_family="AT_rich"
27068. .27289
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1951. .5281
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                               family="(TA)n"
2. .25500
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5. .23830
                                                                                                                                       _family="MER69"
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Submitted (10-AUG-2000) Nobuyoshi Shimizu, Keio University, Sc
Submitted (10-AUG-2000) Nobuyoshi Shimanomachi, Shinjuku-ku,
of Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku,
160-8892, Japani (E-mail:nshimizu@dmb.med.keio.ac.jp,
Tel:81-3-3351-2370, Fax:81-3-3351-2370)
On Jan 19, 2001 this sequence version replaced gi:9798632.
                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 183125)
Shimizu, N. and Asakawa, S.
Homo sapiens chromosome clone KB1670H7 on 8q23
Published Only in DataBase (2000) In press
2 (bases 1 to 183125)
Shimizu, N. and Asakawa, S.
                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens genomic DNA, AP002848
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33152. .33240
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/rpt_family="MIR"
27834...28144
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complement(27340.
/rpt_family="L2"
                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="8"
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complement(33832.
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                             /map="8q23"
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28499. .28616
               /clone="KB1670H7"
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cell_line="FLEB 14 -
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/rpt_family="Li" .1990) complement(1918819990) /evidence-not_experimental /rpt_family="HERV16"	/evidence-not_experimental /rpt_family="MIT72E" complement(1788418823) /evidence-not_experimental	/evidence-not_experimental /rpt_family="MUTIA2" 1796. 17878	1705417186 /evidence-not_experimental /rpt_family="MLT2E" 1718717595	/TPC_taml1y="MJT1H" 1674616902 /evidence=not_experimental /rpt_family="MER5A"	/evidence=not_experimental /rpt_family="MLTlB" complement(15944 . 16116) /evidence=not_experimental	<pre>complement(1517615653) /evidence=not_experimental /rpt_family="L1PA2" complement(1566615940)</pre>	/fpt_idml1y="\2" 14820. 14998 /evidence=not_experimental /rpt_family="MLTIH"	/rpt_family="MIR" complement(1457914677) complement(1457914677) /cvidence=not_experimental	/evidence=not_experimental /rpt_family="12" /complement(1430714557) /evidence=not_experimental	/evidence=not_experimental /rpt_family="MIR" complement(13969. 14098)	/evidence=not_experimental /rpt_family="(TC)n" complement(1375213836)	1177611956 117761956 /evidence=not_experimental /rpt_family="MIR" 13213 13213	/rt_family="AluSx" /rpt_family="AluSx" 10799. 10895 /evidence=not_experimental /ret_family="12"	/evidence-not_experimental /rpt_family="L2" 10507, 10798	<pre>complement(98249923) /evidence=not_experimental. /rpt_family="MIR" 10506</pre>	/rpt_family="HERVL" complement(72158911) /evidence=not_experimental /rpt_family="HERVL"	/evidence=not_experimental /rpt_family="12" complement(5870: .7113) /evidence=not_experimental	/evidence=not_experimental /rpt_family="LIPA13" complement(56515736)	<pre>/clone_lib="Keio BAC library" complement(1191004)</pre>
repeat_region repeat_region	repeat_region	repeat_region		repeat_region	repeat_region	repeat_region	repeat_region		repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region repeat_region	repeat_region	repeat_region	repeat_region
complement(3341433633) /evidence=not_experimental /rpt_family="MIR" complement(3378234282)	/rpt_ramily="L2" 3226132348 /evidence=not_experimental /rpt_family="MIR"	/ryt_family="AT_rich" 3138431512 /evidence=not_experimental	/evidence=not_experimental /rpt_family="Aludb" 3086130888 /evidence=not_experimental	<pre>complement(3004030244) /evidence=not_experimental /rpt_family="MIR" complement(3028030581)</pre>	<pre>/rpt_family="Aluy" 2973129753 /evidence=not_experimental /rpt_family="(TTTTG)n"</pre>	/evidence=not_experimental /rpt_family="MER70A" 2918329494 /evidence=not_experimental	<pre>complement(2803828300) /evidence=not_experimental /rpt_family="MLTIK" complement/28397 28851)</pre>	27830. 27862 /evidence=not_experimental /rpt_family="AT_rich"	<pre>/rpt_iamily="L2" complement(2752827609) /evidence=not_experimental /rpt_family="L2"</pre>	/rpt_family="MLT1J" 2741927524 /evidence=not_experimental	/evidence=not_experimental /rpt_family="MLT2G" 2718027403 /evidence=not_experimental	/evidence=not_experimental /rpt_family="MLT1J" 2676727179	complement(2644326521) /evidence=not_experimental /rpt_family="MADE1" 26762	/evidence=not_experimental	/evidence=not_experimental /rpt_family="(CA)n" 2285322873	22760	<pre>/rpt_family="LTR16A" complement(21559 . 21801) /evidence=not_experimental /rpt_family="HALL1"</pre>	/ryt_family="HERV16" /rpt_family="HERV16" complement(21009 . 21269) /evidence=not_experimental	<pre>complement(2041221003) /evidence=not experimental</pre>

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                               Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Barkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Graham, L., Grand-Pierre, N., Levine, R., Lieu, C., Liu, G., Macdonald, P., Marquis, N., McCarthy, M., McBwan, P., McKernan, K., McPwan, P., McKernan, K., McPwan, P., McReira, 
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       Strauss, N., Tirrell, A.,
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Birren, B., Linton, L., |
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/rpt_family="MIR"
complement(37413. ..37458)
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35473. .35652
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/rpt_family-"L1PA2"
complement(34414. .34574)
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/rpt_family="MIR"
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               Talamas, J., Tesfaye, S.,
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12
                            Theodore, J.,
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Zimmer, A. and Zody, M.
Direct Submission
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----- Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L10840
Center clone name: 1059_L_18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www-seq.wi.mit.edu
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Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J Institute/MIT Center for Genome bridge, MA 02141, USA

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastlen,V., BoguslavKiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,

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Submitted (01-FEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 1, 2002 this sequence version replaced gi:18450000. All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

Center: Whitehead Institute/ MIT Center for Genome Research

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complement/10000
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complement/150?
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AUTHORS
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Best Local Similarity:
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E2 (bases 1 to 195477)

E3 Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukpalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., Eritzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Graham, L., Grand-Pierre, M., Johnson, R., Jones, C., Kann, L., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Levine, R., Lieu, C., Liu, G., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McKernan, K., McPwan, P., McKernan, K., Pierre, N., Pisani, C., Pollara, Y., Norman, C.H., O'Connor, T., Peterson, K., Pierre, N., Pisani, C., Pollara, Y., Raymond, C., Rieback, M., Riley, R., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Wo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J.,
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Homo sapiens chromosome 8 clone RP11-480F5 map 8, WORKING DRAFT
SEQUENCE, 23 unordered pieces.
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Unpublished
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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Matches:
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COMMENT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing vector: Plasmid: n/a; 100% of read Sequencing vector: Plasmid: n/a; 100% of read Chemistry: Dye-terminator Big Dye; 100% of re Assembly program: Phrap; version 0.960731 Consensus quality: 180424 bases at least Q40 Consensus quality: 18415 bases at least Q30 Consensus quality: 191442 bases at least Q20 Consensus quality: 191442 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert size: 198000; agarose-fp
Insert size: 193277; sum-of-contigs
Quality coverage: 4.2 in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: WIBR
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1877 1976: gap of 100 bp
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(8987 59086: gap of 100 b
9087 60289: contig of 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             776 875: gap of
876 1876: cr
                                                                                                                                                                       65 77864: gap of 100 bp
65 81116: contig of 3252 b
165 81216: gap of 100 bp
17 85155: contig of 3939 b
18 85255: gap of 100 bp
18 89134: contig of 3879 b
                                104917: gap of 100 bp
118601: contig of 13684 k
118701: gap of 100 bp
119776: contig of 11075 k
                                                                                                                                     89234: gap of 1
96530: contig of
                                                                                                                                                                                                                                                                                                72002: gap of
74471: contig of
74571: gap of
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61513: contig of 1124
13: gap of 100 b
62903: contig of 1290
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/db_xref="taxon:9606"
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74572. .77764
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KEYWORDS
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                                                                                             TITLE
JOURNAL
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                                                                                                                                                                                                                        Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovař, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Mahshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Ovledo, R., Pace, A., Payton, B., Peery, J., Perez, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rolfeys, M., Rojas, A., Rojubokan, L., Rolfey, H., Stone, H., Stone, H., Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Stone, H., Sotton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, N., Thomas, S., Ward, Moore, S., Warren, R., Washington, C., Watliamson, A., Williamson, A., Wilczyk, R., Wooden, S., Worley, K., Wu, Y., F., Zhou, J., Zorrilla, S., Nelson, D., Weinston, G., Milliamson, A., Thomas, S., Worley, K., Mu, Y., F., Zhou, J., Zorrilla, S., Nelson, D., Weinston, S., Wolley, R., Shou, J., Zorrilla, S., Nelson, D., Weinston, D., Williamson, A., Thomas, S., Wolley, K., Mu, Y., F., Zhou, J., Zorrilla, S., Nelson, D., Weinston, D., Williamson, A., Williamson, A., Willecyk, R., Wooden, S., Worley, K., Wu, Y., F., Zhou, J., Zorrilla, S., Nelson, D., Weinston, D., Williamson, A., Williamson, A., Williamson, M., Williamson, M.
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Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Davila,M.L., Davis,C., Davy-Carroll,L., Ding,Y., Dinh,H.H.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwalte,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes, A., Hernandez,I.
Direct Submission
Submitted (08-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 91382)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N
Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carron, T.F., Carter, M., Cavasos, S.R., Chacko, J., Chavez, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC109887 91582 bp D. Rattus norvegicus clone CH230-312G3, ***, 49 unordered pieces.
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Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
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IN PROGRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 12, 2002 this sequence version replaced gi:18860208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 49 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap: version 0.990329 Consensus quality: 62571 bases at least Q40 Consensus quality: 66037 bases at least Q30 Consensus quality: 69135 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Baylor College of Medicine
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TITLE
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Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,

Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,

Falls, T., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,

Gobisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,

Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,

Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,

Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,

Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,

Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,

Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,

Karlsson, E., Kelly, S., Khan, U., King, L., Koryah, J., Kovar, C.,

Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,

Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.,

Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,

Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,

Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,

Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, N., Nguyen, N.,

Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogdh, M., Okwuonu, G.,

Oraaning and Martine, A., Davron, B., Deery, I., Derez, L.,

Perez, L., L.,

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                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (17-5EP-2001) Human
of Molecular and Human Genetic
Baylor Plaza, Houston, TX 7703
3 (bases 1 to 169845)
Submitted (11-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Direct Submission
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Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, Chen, S., Chen, R., Chen, R., Chowdhry, I., Christopoulos, Chen, S., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, Chen, S., Chen, R., Chen, R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleost
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barbaria, J., Benton, J., Bimage, K., Blankenburg, K.,
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of Medicine, One
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Bryant,N.P.,
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COMMENT
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NOTE: This is a 'working draft' sequence. It currently consists of 67 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jul 10, 2002 this sequence version replaced gi:20975871.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reasonably program: Phrap; version 0.990329
Consensus quality: 104990 bases at least Q40
Consensus quality: 112511 bases at least Q30
Consensus quality: 112479 bases at least Q20
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Center clone name: CH230-9A18
Center clone summary Statistics
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Contact: hgsc-help@bcm.tmc.edu
Project Information
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Web site: http://www.hgsc.bcm.tmc.
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Submitted (10-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 9, 2002 this sequence version replaced gi:17941726.
                                                                                                                                                                                                                                                                                                                    Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 191204)
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, *** SEQUENCING IN PROGRESS ***,
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arbitrary. Caps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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NOTE: This is a 'working draft' sequence. It currently
consists of 76 contigs. The true order of the pieces
is not known and their order in this sequence record is
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Contact: hgsc-help@bcm.tmc.edu
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Rattus norvegicus clone CH230-9L22,
60 unordered pieces.
                       Baylor Plaza, Houston, Tx //טיט, יייה on Jul 11, 2002 this sequence version replaced gl:17942447 on the following center genome Center
                                                                                                                                                                                                                                                Submitted (16-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                 Submitted (12-JUL-2002) Human Genome Sec
of Molecular and Human Genetics, Baylor
Baylor Plaza, Houston, TX 77030, USA
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Center, Department of Medicine, One

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NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a "vorking draft" sequence. It currently
consists of 60 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 44880 bases at least 040
Consensus quality: 54834 bases at least 020
Consensus quality: 562109 bases at least 020
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Mus musculus clone RP24-576L9,
                                                                                                                                                                                                                                                                      Submitted (20-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 20, 2002 this sequence version replaced gi:17060976. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Contact: sequence_submissions@genome.wi.mit.edu
                                                     Web site: http://www-seg.wi.mit.edu
                                                                                                                 Center: Whitehead Institute/ MIT Center Center code: WIBR
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3718:
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5222:
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NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as soon as it is available and the accession number be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insert.size: 157000; agarose-fp
Insert size: 171455; sum-of-contigs
Quality coverage: 12.8 in Q20 bases; agarose-fp
Quality coverage: 11.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assembly program: Phrap; version 0.960731 Consensus quality: 169439 bases at least Q40 Consensus quality: 170530 bases at least Q30 Consensus quality: 170959 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads
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Center clone name: 576_L_9
                                                                                                                                                                                                                                                   /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP24-576L9"
                                      note="assembly_fragment"
                                                                                                                                                                                        note="assembly_fragment"
                                                                                                                                                                                                                                 clone_lib="RPCI-24 Male Mouse BAC"
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89723: contig of
89823: gap of 1
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contig of 661 bp in length
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RESULT 13
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Best Local Similarity:
Query Match:
                                    DEFINITION
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            Rattus norvegicus clone CH230-501B21, ***, 30 unordered pieces.
                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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X61200
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Identification of genes differentially expressed in two types v-myb-transformed avian myelomonocytic cells

Oncogene 7 (3), 527-534 (1992)
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Submitted (01-AUG-1991) T.H. Graf,
AC118327
AC118327.2 GI:21747379
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/note="assembl
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198 c 129 g 113 t
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                                                                                                                                                                                                                                                                                                       /organism="Gallus gallus"
/db_xref="taxon:9031"
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Conservative:
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Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Homsi,F., Howard,S., Hubber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
Lozado,R.J., Lu,X., Lucler,A., Lucler,R., Luna,R., Ma,J.,
Lozado,R.J., Lu,X., Lucler,A., Lucler,R., Martindale,A., Martinez,E.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Morgan,M., Morris,S.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Rultz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,K., Tang,H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (14-JUL-2002) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA On Jul 14, 2002 this sequence version replaced 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (15-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA.

3 (bases 1 to 139754)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H. Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, C., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
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Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R. Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                              Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
-----Project Information
                                                                                                                                       Center project name: GVZL Center clone name: CH230-501B21
                                           Sequencing vector: Plasmid;
                                                                                                                                                                                                                                                                                                                                                                          Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Baylor College of Medicine
Dye-terminator Big Dye:
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Rodentia;
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Bryant,N.P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thomas, S.,
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runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assembly program: Phrap; version 0.990329
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Consensus quality: 120062 bases at least Q30
Consensus quality: 122808 bases at least Q20
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Best Local Similarity:
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Douthwaite, K. J., Draper, H., Duyan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Garcia, J., Hart, M., Havlak, P., Hawes, A., Hennandez, J.,
Harris, K., Hart, M., Havlak, P., Hawes, A., Hennandez, J.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Jackson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Karlsson, E., Kelly, S., Khan, U., Lieu, C., Liu, W., Louiseged, H.,
Lozado, R.J., Lu, X., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louiseged, H.,
Lozado, R.J., Lu, X., Lucier, R., Luna, R., Ma, J.,
Maheshwari, M., Mapha, P., Martin, R., Martindale, A., Martinez, E.,
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
Mossey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mgyen, A., Ngyen, N.,
Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G.,
Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
Peters, L., Pikens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y.,
Rives, M., Rojas, A., Rojubokan, J., Rolfe, M., Ruiz, S., Savery, G.,
Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I.,
Sutton, A., Svatek, A., Tandor, P., Tamerisa, K., Thomas, N., Thomas, S.,
Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, O.,
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Buhay, C., Burch, P., Burkett, C.S., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, R., 
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Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.
Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
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Center: Baylor College of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williamson,A., Wieczyk,R., Wooden,S., Worley,K., Wu.C., Wu.Y., Wu.Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.
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                                                                                                                                                                                                                                                                            NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a "vorking draft' sequence. It currently consists of 85 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 79000 bases at least 040
Consensus quality: 85421 bases at least 030
Consensus quality: 90756 bases at least 020
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                                                                                                                                                                                                                                                            CE 2 (bases 1 to 174354)

RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Roderson, S., Barna, M., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campoplano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McKernan, K., Meldrin, J., Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nuylen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stolanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tasfaye, S., Theodore, J., Tayland, N., Jembek, L., Zimmer, A. and Zody, M.
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3 SerIleLeuCysSerProLeuProSerLeuSerLeuSer 15
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Mus musculus, clone RP23-232G11
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Mus musculus clone RP23-232G11,
                                                                                                                                                                                                          Submitted (31-JAN-2002) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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Birren, B., Linton, L., 
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L.,
Mihova,T., Mlenga,V., Murphy,T., NayJor,J., Nguyen,C., Nicol,R.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Jainoun, T., James, A., and Jode, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (25-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On APR 25, 2002 this sequence version replaced gi:18450091. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://ftp.genome.washington.edu/RM/RepeatMasker.html
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MacLean,C., Macdonald,P., Major,J., Marquis,N., Matt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by the finished sequence as soon as it is available and the accession number will be preserved.

1 101: contig of 101 bp in length
102: 201: gap of 100 bp
202 1145: contig of 944 bp in length
1116 1245: gap of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              provided by the submittor. This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
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Insert size: 17234; sum-of-contigs
Quality coverage: 5.7 in Q20 bases; agarose-fp
Quality coverage: 6.0 in Q20 bases; sum-of-contigs
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Consensus quality: 165923 bases at least 040
Consensus quality: 169611 bases at least 030
Consensus quality: 171268 bases at least 020
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4067 4166: gap of 100 bp
4167 5725: conti
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8139
                                                                                                      167 4166: gap of 100 bp 167 1579 bp 17 1579 
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99: gap of 100.bp
31892: contig of 4293 1
92: gap of 100 bp
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BASE COUNT
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53673 66319: contig of 12647 bp in length

66320 66419: gap of 100 bp

66420 80154: contig of 13735 bp in length

80155 80254: gap of 100 bp

80255 94472: contig of 14218 bp in length

94473 94572: gap of 100 bp

94573 120577: contig of 26005 bp in length

120578 120677: gap of 100 bp

120678 147069: contig of 26392 bp in length
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7170 174354: contig of 27185
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147170. .174354
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39544 c 39585 g
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/db_xref="taxon:10090"
/clone="RP23-232G11"
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20678. .147069
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lone_end:SP6
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37390: gap of 100 bp
45486: contig of 8096 bp in length
45586: gap of 100 bp
53572: contig of 7986 bp in length
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6420...80154
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6885. .20475
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1673. .66319
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5587. .53572
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contig of 7986 bp in length
                                                   46362 t
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                                                   2055 others
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Search completed: July 1, 2003, 00:18:12 Job time: 249:866 secs

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Command line parameters:

-MODEL-frame+_p2n.model -DEV-xlp
-MODEL-frame+_p2n.model -DEV-xlp
-Q-/cgn2_1/USPTO_spoo1/US10075846/runat_25062003_163647_5141/app_query.fasta_1.782
-DB-N_Geneseq_101002 -QFMY=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END--1 -MATRIX=blosum62 -TRANS=human40.cdi
-LISY=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN-0 -MAXIEN-200000000
-USER-US10075846_@CGN_1_1_511_@runat_25062003_163647_5141 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum DB
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Maximum Match 100%
Listing first 45 s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
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    nucleic search, using frame_plus_p2n model

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length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N_Geneseq_101002:*

1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*

2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Egapop 6.0 , Egapext Delop 6.0 , Delext
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                 BLOSUM62
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5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
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/SJDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
/SJDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
/SJDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
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Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pu and is derived by analysis of the total score distribution.
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Result No. Score 47 47 47 Query Match 69 69 90 70 70 3171 112460 249487 288 576 668 668 668 698 730 73271 4010 5412 10468 110468 110468 110468 110468 110468 110468 Length 3599 20453 418 471 3301 90 90 90 597 DΒ ij ABK83567 ABN85733 ABK82060 ABK82062 AAC6168: AAD17468 ABA75659 AAQ48939 AA19499 ABK73574 AAL16141 ABV46523 ABV16725 ABL03244 ABA63211 AAK9064 AAS4200: ABL26393 SUMMARIES Human immune/haema Human digestive sy Drosophila melanog Human breast cance Novel floral meris Novel floral meris Novel floral meris DNA encoding novel DNA encoding novel Human reproductive Human reproductive Genomic sequence # DNA encoding novel Arabidopsis thalia DNA encoding novel DNA encoding novel DNA encoding novel Human cDNA differe Mouse genomic regi Human breast cance Human breast cance Bacillus lichenifo Human immune/haema Human neuroblastom Human neuroblastom Arabidopsis thalia Human G-protein co Rat aorta range pr Human BAI2 gene. Human prostate exp Human prostate exp Rat kd312 polypept Rat kd312 genomic Human transporter Drosophila melanog Human prostate exp Human prostate exp Description Human brain expres Probe #8168 for ge Human brain expres Probe #17300 for g Human foetal liver Human PPAR-delta Steroid hormone Nucleotide sequenc cancer PPAR-delta c cancer relate foetal liver

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RESULT 1
AACC16A1
ID AACC6
XX
AC AACC6
XX
AC AACC6
XX
NO 19-F
XX
KW Huma
XX
KW Huma
XX
KW Homc
XX
KW Homc
XX
FT exon
                                              Homo
                                                                                                                                     AAC61681 standard;
                                                               Human; ataxia;
                                                                                Nucleotide sequence of the human ataxia
                                                                                                  19-FEB-2001
 intron
                                              sapiens
                                                                                                  (first entry)
                                                               gene
                  Location/Qualifiers
29850..29921
/*tag= a
29922..33025
                                                                                                                                     DNA;
                                                               therapy;
                                                                                                                                      39796
                                                                                                                                      ВΡ
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ALIGNMENTS

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RESULT 2
AAQ48939
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score:
AAQ48939;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents the human ataxia gene. The ataxia protein and polynucleotides are useful for diagnosing and treating disorders related to ataxia. Ataxia gene sequences are useful in gene therapy, and as diagnostic tools or reagents for identifying and characterizing genetic defect involved in the disorders and diseases related to ataxia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exon
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                                                       AAQ48939 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 39796 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acid sequence encoding human ataxia protein for screening compounds useful for treating disorders relating to mutations in ataxia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-656166/63.
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                                                                                                                                                               Page 22-44; 47pp; English.
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68.00
100.00%
93.33%
90.67%
21
                                                       DNA;
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                                                       3294 BP
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                                                                                                                                                                                                                                                                                                                               Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
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RESULT 3
AAX36523
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.:
        06-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3294 BP; 705 A; 1014 C; 879 G; 696 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human steroid hormone receptor NUCI - used evaluate ligands binding to the receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                      Nuclear receptor agonist; antagonist; identification; peroxisome proliferator activated receptor; ss.
                                                                                                                                          Human PPAR-delta coding sequence.
                                                                                                                                                                                            AAX36523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                The steroid hormone receptor (designated NUCI) is used in assays to identify and evaluate chemical entities that bind to it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Page 6-8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAR41875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1993-305586/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rodan GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-MAR-1992;
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                                                        WO9918124-A1
                                                                               Homo sapiens
                                                                                                                                                                                                                   AAX36523 standard; cDNA; 3301 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-1993;
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                                 15-APR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                     1837
                                                                                                                                                                                                                                                                 hormone receptor (NUCI) gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hormone;
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        98WO-US21049.
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/product= Steroid hormone receptor
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07-OCT-1997;

97US-0061385

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RESULT 4
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05-JUN-2000

05-JUN-2000

18-SEP-2000

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20-SEP-2000

20-SEP-2000

20-SEP-2000

22-SEP-2000

22-SEP-2000

25-SEP-2000

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25-SEP-2000
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                                                                                                                                                                                                                                      Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcin
                                                                                                                                                                                                                                                                                Lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence encodes the human peroxisome receptor-delta (PPAR-delta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
                                                                                                                                              30-MAY-2001;
                                                                                                                                                                   13-DEC-2001.
                                                                                                                                                                                      WO200194629-A2
                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                     15-MAY-2002
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                                                                                                                                                                                                                                                                                                                                             ABL65244 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3301 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antagonist of nuclear receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying nuclear receptor agonists
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P-PSDB; AAY05472.
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                                                                                                                                                                                                                                                                                 cancer
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2000US-234034P.

2000US-234052P.

2000US-234509P.

2000US-234567P.

2000US-234924P.

2000US-234924P.

2000US-235077P.

2000US-235072P.
                                                                                                                                                                                                                                                                                related
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                                                                                                               2000US-209473P.
2000US-209531P.
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                                                                                  2000US-234009P.
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Query Match:

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Length:
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Alignment Scores:

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US-10-075-846-4_COPY_192_207 (1-16)

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ABL65244 (1-3301)

Gaps: Mismatches: Indels:

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CC expression of at least one gene (I) of a signature gene set, where (I) CC expression of at least one gene (I) of a signature gene set, where (I) CC comprises a sequence (S) selected from 8447 sequences (given in ABL6164 CC of ABL70110), or is at least 95% identical to (S), where a change in CC expression is indicative of anti-neoplastic activity. (I) has cytostatic cativity and can be used in gene therapy. M1 can be used for screening CC an anti-neoplastic agent, and can be used for producting a product which is the data collected with respect to the anti-neoplastic agent as a CC result of M1, and the data is sufficient to convey the chemical CC structure and/or properties of the agent. M1 can be used in the CC treatment of cancer such as colon, breast, stomach, lung, thyroid, CC oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine corcinoma, papillary carcinoma and Wilm's tumour.
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02-OCT-2000
02-OCT-2000
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28-SEP-2000;
28-SEP-2000;
28-SEP-2000;
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26-SEP-2000;
27-SEP-2000;
27-SEP-2000;
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Soppet DR,
                                                                                                                                                                                                                                  The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change i expression of at least one gene (I) of a signature gene set, where (I)
                                                                                                                                                                                                                                                                                                                                          Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene
                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID 3581; 44pp; English.
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29-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Augustus
Weaver Z
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2000US-237316P.
2000US-237425P.
2000US-23759BP.
2000US-237604P.
2000US-237606P.
2000US-237608P.
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2000US-236891P.
2000US-237172P.
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2000US-237294P
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2000US-236109P.
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705 A; 1014 C; 879 G; 696 T; 7 other;
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ID ABA75659
                    AAK24269/c
                                                                                                                                                             Alignment Scores:
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                                                                                                                                                                                             The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                 03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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26-MAY-2000;
30-JUN-2000;
          AAK24269
                                                                                                                                                                                Sequence 90
                                                                                                                                                                                                                                                                                           Claim 4; SEQ ID NO 23964; 639pp + sequence listing;
                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                            Penn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human foetal liver single exon nucleic acid probe #23964.
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                                                                 SerIleLeuCysSerProLeuProSerLeuSerLeuSer
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                                               TCGCTATCTTGCTCTCCTCTCTCTCTCTCTCTCC
                                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
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2000US-0207456
2000US-0608408
2000US-0632366
2000US-0632368
2000US-0236359
2000US-0236359
2000US-0236353
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Matches:
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Best Local Similarity:
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
cervical cancer;
       Probe; human; microarray;
                           Probe #17300
                                             12-OCT-2001
                                                                                   AAI27367
                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                             Single
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                                                                                   standard;
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0236359.
2000US-0236359.
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52.00
92.31%
76.92%
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probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exon nucleic acid probes
                                                                                                                                                                                                                                                          SerIleLeuCysSerProLeuProSerLeuSerLeuSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expressed single exon
                                         for gene expression analysis in human cervical cell sample
  gene expression;
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Matches:
Conservative:
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cervical epithelial cell;
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                                                                                                                                                                                   RESULT 8
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21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Penn
                                                                                                                                                                                                                                                                                                                                                              Sequence 90 BP;
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                                                                                                                                                              ABA63211 standard;
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30-JUN-2000;
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                                WO200157277-A2
                                                     Homo
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                                                     sapiens
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zing gene expression in human cervical epithelial cells
                                                                                             foetal liver single exon nucleic acid probe #11516.
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                                                                         foetal
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0234687.
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                                                                                                                                                               597
                                                                        expression;
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Matches:
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AAK11674/c
ID AAK11674 s
XX
AC AAK11674;
XC AAK11674;
XX O5-NOV-200
XX Human brai
XX Human; brai
XX Human; brai
XX Human; brai
XX Homo sapi
XX epilepsy;
XX Homo sapi
XX O9-AUG-200
XX O9-AUG-200
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PR 30-JAN-200
PR 30-AUG-200
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 26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
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21-SEP-2000;
27-SEP-2000;
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                        microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                   AAK11674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
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                                        04-FEB-2000;
                                                                                                                                                                                                    Human; brain expressed exon;
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                                                                    30-JAN-2001; 2001WO-US00667
                                                                                                                        WO200157275-A2
                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                               Human brain expressed single exon probe SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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Matches:
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27-SEP-2000;
04-OCT-2000;
WPI; 2001-488901/53
                                                                                                                                                                                                                                                                                                                                                                                      probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                30-JUN-2000;
03-AUG-2000;
                                                                               04-FEB-2000;
26-MAY-2000;
                                                                                                                   09-AUG-2001.
                                                                                                                                  WO200157278-A2
                                                   21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                                    Probe
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                             (MOLE-)
                                                                                                                                                 Homo sapiens
                                                                                                                                                               cervical
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                                                                                                                                                                    human; microarray; gene expression; cervical epithelial cell;
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                            MOLECULAR DYNAMICS
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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2000US-0236359.
2000GB-0024263.
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52.00
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Matches:
Conservative:
Mismatches:
Indels:
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Pred
              Alignment Scores:
                                                                                                         from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.
                                        Sequence
                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                     The
                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                             analyzing
                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes
                                                                                                                                                                                                  The present invention relates to human single exon nucleic (SENP). The present sequence is one such probe. The SENPs a
                                                                         ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                 8168; 487pp;
                                                                                                                                                                                                                                                                              in human cervical epithelial cells
                                          C;
                                          116
                                                                                                                                                                                                                                                  English.
                                          <u>ი</u>
                                          178
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                                            other;
                                                                                                                                                                                                                                                                                             useful for
                                                                                                                                                                                                   acid probe
are derived
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AAD17468/
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Best Local Similarity:
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                          25-FEB-2000;
02-MAR-2000;
09-MAR-2000;
17-MAR-2000;
24-MAR-2000;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                               cystic fibrosis; Alzheimer's disease; depression; epilepsy; scleroderma; cardiomyopathy; muscular dystrophy; Crohn's disease; multiple sclerosis; rheumatoid arthritis; cancer; anaemia; asthma; trauma; haemodialysis;
                                                                                                                                       23-FEB-2001;
                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                    Homo
                                                                                                                                                                                                                                                                                                                                                                                                             neurological disorder; immune disorder; allergy; nootropic; de
AIDS; Acquired Immune Deficiency Syndrome; amyotrophic lateral
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AAD17468 standard;
(INCY-) INCYTE
                                                                                                                                                                         30-AUG-2001.
                                                                                                                                                                                                     WO200162923-A2.
                                                                                                                                                                                                                                                                                                                                                  gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human;
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                                                                                                                                                                                                                                                                                                                  sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               transporter and ion channel;
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                                                                                                                                                                                                                                                                                                                                                  inflammation;
                            ; 2000US-0184866.
; 2000US-0187947.
; 2000US-0188333.
; 2000US-0190230.
; 2000US-0192077.
; 2000US-0193500.
                                                                                                                                         2001WO-US05942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
GENOMICS INC
                                                                                                                                                                                                                                                                    Location/Qualifiers 221..1168
                                                                                                                                                                                                                                   /product=
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52.00
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76.92%
69.33%
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                                                                                                                                                                                                                                    "Human TRICH-1 protein"
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Matches:
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ABL03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a cDNA encoding human transporters and ion channels (TRICH-1) protein. The TRICH DNA, protein and their agonist antagonists are useful in the diagnosis, treatment and prevention of transport disorders (akinesia, amyotrophic lateral sclerosis, cystic fibrosis), neurological (Alzheimer's disease, dementia, depression, epilepsy), muscle (e.g. cardiomyopathy, Becker's muscular dystrophy) immunological disorders (e.g. allergies, acquired immunodeficiency syndrome (AIDS), Crohn's disease, rheumatoid arthritis, sclerosland multiple sclerosls), viral, bacterial, parasitic, protozoal and helminthic disorders, cancer, anaemia, asthma, trauma, haemodialysis,
                                                                                                                                                                                                                                                                                                                 3244/c
ABL03244 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yue H,
Khan FA,
         P-PSDB; ABB59141
                                                                                      23-MAR-2000;
11-JUL-2000;
                                                                                                                       23-MAR-2001; 2001WO-US09231
                                                                                                                                               27-SEP-2001.
                                                                                                                                                                      WO200171042-A2
                                                                                                                                                                                          Drosophila melanogaster
                                                                                                                                                                                                                  pharmaceutical;
                                                                                                                                                                                                                             Drosophila;
                                                                                                                                                                                                                                                Drosophila melanogaster expressed polynucleotide SEQ ID NO 4214.
                                                                                                                                                                                                                                                                         26-MAR-2002
                                                                                                                                                                                                                                                                                                ABL03244;
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                                           Venter JC,
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                    2001-656860/75
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                                                                CORP NY.
                                                                                                                                                                                                                            developmental biology;
                                         Adams M,
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2000US-0614150
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Gandhi AR, Tribo
BD, Hernandez R,
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Matches:
Conservative:
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Indels:
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RESULT 13
ABV16725/c
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                17-FEB-2000;
16-MAR-2000;
25-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                capable of detecting 1000 or more genes from Drosophila. The inventuaseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                        Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                Human prostate expression marker cDNA 16716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABV16725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABV16725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid genes from Drosophila and
                                                                                                      Schlegel
                                                                                                                                                                                   09-JUN-2000;
                                                                                                                                                                                                                                                    20-FEB-2001;
                                                                                                                                                                                                                                                                              23-AUG-2001
                                                                                                                                                                                                                                                                                                       WO200160860-A2
                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                           13-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ABB57737-ABB72072)
                                                                                                                               (MILL-) MILLENNIUM PREDICTIVE MEDICINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerSerSerIleLeuCysSerProLeuProSerLeuSerLeuSer
                                                                                                                                                      2000US-183319P.
2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-219007P.
2000US-255281P.
                                                                                                    Endege WO,
                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                    2001WO-US05171
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51.00
80.00%
66.67%
68.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             418
                                                                                                      Monahan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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Matches:
Conservative:
Mismatches:
Indels:
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Claim 1; Page 2785; 11750pp; English.

Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.

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Best Local Si
Query Match:
DB:
*355555555555555555555555
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Best Local Similarity:
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                                                                                                                                                                                               09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
              Claim
                                       Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, usef for detecting presence of prostate cancer, stage of prostate cancer
                                                                                                                                                                                                          17-FEB-2000; 2000US-183319P.
16-MAR-2000; 2000US-189862P.
25-MAY-2000; 2000US-207454P.
09-JUN-2000; 2000US-211314P.
18-JUL-2000; 2000US-219007P.
                                                                                                                                                                                                                                                                                                                                                                                                                          Human; prostate pharmacogenomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                    Schlegel
                                                                                                                                                                                                                                                                                                                                                                   WO200160860-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human prostate expression marker cDNA 46514.
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              Page 9177; 11750pp; English
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marker;
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50.00
92.86%
64.29%
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                                                                                                                                                                                                                                                                                                                                                                                                                          gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                       cytostatic; carcinogen;
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                                                                                                                                                                 MEDICINE
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        pharmacodyanamic marker;
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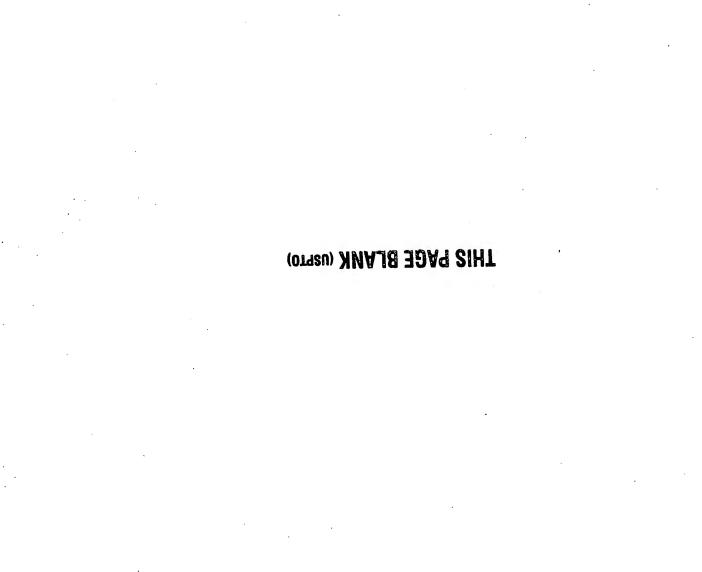
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                                                                                                                                                                                                                                                                                                         XFXPD
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(a) assessing whether a patient is affilicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a patient;
          The invention provides nucleic acid molecules encoding human and rat Kd312 polypeptides. The kd312 polypeptides can be expressed by standard recombinant methodology. The kd312 sequences, and the antibodies against the proteins may be used to treat or diagnose the presence or progressic
                                                                                            Claim
                                                                                                                          kd312 polypeptides useful for treating diseases and disorders associated with alterations in cell proliferation and cell de
                                                                                                                                                                                                                           Yen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat kd312 polypeptide encoding
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                                                                                                                                                                                          WPI; 1999-601322/51.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kd312 polypeptide;
heart attack; head
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ23024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  tide; cancer; immunodeficiency disorder; AIDS; stroke;
head trauma; neurodegenerative disease; rat;
isease; Alzheimer's disease; ss.
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                                                                                            English.
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Matches:
Conservative:
Mismatches:
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diseases,

cancer,

immunodeficiency

or progression rs (e.g. AIDS), against



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Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp
-MODEL=frame+_p2n.model -DEV=xlp
-Q-cgn2_1/USPTO_spool/US10075846/runat_25062003_163649_5167/app_query.fasta_1.782
-DB-Issued_Patents_NA -QFMT=fastap -SUFFIX-p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS-humand0.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10075846_@CGN_1_1_84_erunat_25062003_163649_5167 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -DSPBLCCK=100 -LONCLOG
-DEV_TIMEOUT=120 -NARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                               Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq length: 0 seq length: 2000000000
 Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Match Length
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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US-09-053-374A-6
US-09-053-806-1
US-09-163-669-1
US-09-179-221D-3
US-09-179-221D-3
US-09-453-702B-70
US-08-254-358-1
US-08-254-358-1
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PCT-US95-07178-1
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ALIGNMENTS

RESULT 1 US-09-053-374A-4

Sequence 4, Application US/09053374A Patent No. 6462177

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/053,374A
                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1689 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: MAMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
ZIP: 91320
                   TOPOLOGY:
                                STRANDEDNESS: single
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                                                 nucleic acid
TYPE:
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                   linear
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                                                                                                                                             31,602
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                               US-08-852-806-1
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
                                              RESULT 3
                                                                                                                                     US-10-075-846-4_COPY_192_207 (1-16) x US-09-053-374A-6 (1-3079)
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US-09-053-374A-6
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Sequence 1, Application US/08852806 Patent No. 5874245
                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-51
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARATERISTICS:
LENGTH: 3079 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: YEN, KWANG-MU
TITLE OF INVENTION: MAMMALIAN BLOOD LOSS-INDUCED GENE, KD312
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                    TOPOLOGY: 11 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
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                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 91320
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US-09-163-669-1
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                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                       Sequence 1, Application Patent No. 6111076
                                                                                                                      GENERAL INFORMATION: APPLICANT: FUKUSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 60/017,91
FILING DATE: 16 MAY 1996
ATTOREY/AGENT INFORMATION:
NAME: HAO, WILLLIAM
REGISTRATION NUMBER: 34,344
REGISTRATION INFORMATION:
TELECOMBUNICATION INFORMATION:
TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: NANTI-SENSE: NO FRAGMENT TYPE:
                               APPLICANT: HINUMA, SHUJI
APPLICANT: FUJII, RYO
TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTOR (HIBCD07)
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Shoji Fukusumi
APPLICANT: Shoji Fukusumi
TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 3271 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   No .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A. ZIP: 19406-0939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 709 Swedeland CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
ADDRESSEE:
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                                                                                                                      FUKUSUMI, SHOJI
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Ratner & Prestia
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Conservative:
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COMPUTER READABLE FORM:

MEDIUM TYPE:

Diskette

COUNTRY: U ZIP: 19482

USA

Valley Forge

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COMPUTER: IBM Compatible OPERATING SYSTEM: DOS

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EARLIER APPLICATION NUMBER: U.S. 60/125,806
EARLIER FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 40
LENGTH: 724
TYPE: DNA
ORGANISM: Homo sapiens
US-09-535-008-40
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Alignment Scores:
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Best Local Similarity:
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                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Wong, Alexander K.C.
APPLICANT: Taytigian, Sean V.
APPLICANT: Taytigian, Sean V.
APPLICANT: Teng, David H.-F.
TITLE OF INVENTION: BRC1 IS A TUMOR SUPPRESSOR THAT IS MUTATED IN PROSTATE
TITLE OF INVENTION: AND OTHER CANCER TYPES
FILE REFERENCE: 2318-259
FILE REFERENCE: 2318-259
CURRENT APPLICATION NUMBER: US/09/535,008
CURRENT FILING DATE: 2000-03-23
CURRENT FILING DATE: 2000-03-23
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 40, Application US/09535008 Patent No. 6465629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 610-407-0700
TELEX: 846169
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 3271 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: TAK+50002-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/163,669 FILING DATE: 30-SEP-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 1 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 610-407-0700
TELEFAX: 610-407-0700
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APPLICATION NUMBER: 08/852,806
FILING DATE: 07-MAY-1997
APPLICATION NUMBER: 60/017,915
FILING DATE: 16-MAY-1996
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Matches:
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Percent Similarity:
Best Local Similarity:
Query Match:
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Sequence 70, Application US/09453702B
Patent No. 6365723
GENERAL INFORMATION:
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US-09-179-221D-3/c
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
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APPLICANT: Musso, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09179221D Patent No. 6291168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NUCLEIC ACID SEQUENCES DIAGNOSTIC FOR PATHOGENIC E.
TITLE OF INVENTION: COLI 0157, METHODS OF IDENTIFICATION AND KIT THEREFOR
FILE REFERENCE: 922.6496p
CURRENT APPLICATION NUMBER: US/09/179,221D
CURRENT FILING DATE: 1998-10-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: No. 6291168epad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1331
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.4
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                 TITLE OF INVENTION: No. 6365723el Sequences NUMBER OF SEQUENCES: 265
                                                                                                                                                                                                                                                                                                                                              APPLICANT: Blattner, Frederick R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   681 GTTCTCTGCTCCCCGGCTCCCTTTTCCACTACCCTC 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 ACATCAATCATCTGTTCTCCAATGACTAGTCTAAAAACTAGTATT 58
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                                                                                                                                                                 CITY: Madison
STATE: WI
                                                                                                                                  COUNTRY: US
ZIP: 53701-2113
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Matches:
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                                                                                                 1.44Mb storage
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CLASSIFICATION: <Unknown>

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US-10-075-846-4_COPY_192_207 (1-16) x US-09-453-702B-70 (1-3191)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08254358
Patent No. 5658785
GENERAL INFORMATION:
APPLICANT: Johnson, Philing
                                                                          NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 70:
                                                                                                                                                                          CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5658785and, Greta E.
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 31,3075
                                 SEQUENCE CHARACTERISTICS:
LENGTH: 4680 base pair
                                                                                               REFERENCE/DOCKET NUMBER: '31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenth Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Ad
TITLE OF INVENTION: ME
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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STRANDEDNESS
                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                     4680 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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Adeno-Associated Virus Materials
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Matches:
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В
US-10-075-846-4_COPY_192_207 (1-16) x US-08-475-391-1 (1-4680)
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Query Match:
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                                                    Query Match:
                                                                                     Percent Similarity:
                                                                                                        Score:
                                                                                                                                       Alignment Scores:
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APPLICANT: Johnson,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                       TELEPHONE: (312) 474-630
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: D. CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 07-JUN-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: No. 5786211and, Gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                         LENGTH: 4680 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               775 ACATCCCCAATTACTTGCTCCCCAAAACCCAGCCTGAGCTCCAGT 819
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                                                                                                                                                                                                                                     nucleic acid
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                                                                                                                                                                                                           linear
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                                                                                                                                                                                      DNA (genomic)
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Matches:
                                                    Mismatches:
Indels:
                                                                                     Matches:
Conservative:
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Query Match:
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US-08-709-609-1
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                                                                                                                                                     Sequence 1, Application PC/TUS9507178 GENERAL INFORMATION:
APPLICANT: Johnson, Philip R.
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TITLE OF INVENTION: Adei
TITLE OF INVENTION: Meti
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERNTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
STREET: COLCAGO
CITY: Chicago
TIllinois
                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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NAME: No. 5858775and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                 ADDRESSEE: Marshall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
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                                                   E: Marshall, O'Toole, Gerstein, Murray & 6300 Sears Tower, 233 S. Wacker Drive
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                                                                                                                   Adeno-Associated Virus Materials and Methods
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RESULT 12
US-08-331-384-2/c
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                                                                                                                                                                             ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION UNMBER: 31,215
REFERENCE/DOCKET NUMBER: UPNG1149USA
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Fisher, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                     CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                  APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
                                                                                                                                COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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TELEFAX: (312) 474-0448
TELEX: 25-3856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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Pennsylvania
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                                                                                                                                                                                    Floppy disk
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William M.
Krishna J.
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                                                                                                                                   Version
                                                                                                                                     #1.25
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RESULT 13
US-08-836-087-2/c
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; MOLECULE TYPE: US-08-836-087-2
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4910 base pairs
                                                                                                                                                  REFERENCE/DOCKET NUMBER: GN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/331,384 FILING DATE: 28-OCT-1994 ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 4910 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                STRANDEDNESS:
                                                                                                                                                                                                  REGISTRATION NUMBER: 31,215
                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Spring House
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                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                  nucleic acid
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Kelley, William M.
Fisher, Krishna J.
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US-10-075-846-4_COPY_192_207 (1-16) x US-09-246-320-2 (1-4910)
                                                            Percent Similarity:
Best Local Similarity:
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                                                                                                                                                         ; STRANDEDNESS:
; TOPOLOGY: unb
; MOLECULE TYPE:
US-09-246-320-2
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Best Local Similarity:
                                             Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                     TELEFAX: 215-540-5818 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION NAME: Bak, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                    TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
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                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                      TYPE: nucleic acid
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Spring House Corpora
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WENTION: Hybrid Adenovirus-AAV Vector and
WENTION: Methods of Use Thereof
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Matches:
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                            ; SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-09-546-738-2
Search completed: July 1, 2003, 00:57:37 Job time: 12.4004 secs
                                                                                                                                                                                                                                                                                                                    Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GNVPN.007PCT
TELECOMMUNICATION INFORMATION:
TELEFAX: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4910 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09546738
Patent NO. 6387368
GENERAL INFORMATION:
APPLICANT: Trustees of University of Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/546,738

FILING DATE: 11-Apr-2000

CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wilson, James M.
Kelley, William M.
Fisher, Krishna J.
Fisher, Krishna J.
TITLE OF INVENTION: Hybrid Adenovirus-AAV Vector and
Methods of Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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                                                                                  2062 ACATCCCCAATTACTTGCTCCCCAAAACCCAGCCTGAGCTCCAGT 2018
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                                                                                                          APPLICATION NUMBER: 09/246,320 FILING DATE: <Unknown>
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STREET: Spring House Corporate Cntr, PO Box 457
CITY: Spring House
STATE: Pennsylvania
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Matches:
Conservative:
Mismatches:
Indels:
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Sequence 13469, A
Sequence 3, Appli
Sequence 11273, A
Sequence 11273, A
Sequence 12894, A
Sequence 7241, App
Sequence 343, App
Sequence 8976, Ap
Sequence 8979, A
Sequence 30770, A
Sequence 30770, A
Sequence 725, App
Sequence 725, App
Sequence 3140, Ap
Sequence 314, App
Sequence 11, Appli
Sequence 11, Appli
Sequence 1, Appli
Sequence 1, Appli

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Title:
Perfect score:
Sequence:
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No.
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-Q-/cgn2_1/USPTQ_spool/US10075846/runat_25062003_163649_5181/app_query.fasta_1.782
-Q-/cgn2_1/USPTQ_spool/US10075846/runat_25062003_163649_5181/app_query.fasta_1.782
-DB-Published_Applications_NA -QFWT-fastap -SUFFIX-p2n.rnpb -MINMATCH-0.1
-LOOPEL-0 -LOOPEXT-0 -UNITS-bits -START-1 -END--1 -MATRX-blosum62
-TRANS-human40.cdi -LIST-45 -DCCALIGN-200 -THR_SCORE-pct -THR_MAX=100
-THR_MIN-0 -ALIGN-15 -MODE-LOCAL -QUTEYT-pto -NORN-ext -HEAGSIZE-500 -MINLEN-0
-MAXLEN-200000000 -USER-US10075846_@CGN_11_1102_@runat_25062003_163649_5181.
-NCPU-6 -ICPU-3 -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLOCK-100
-LONGLOG -DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5
-FGAPOD-6 -FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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Listing first 45 summaries
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                                                                                                                                                                                         : /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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                                                                     Length DB
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 US-10-075-846-3
US-09-938-842A-93
US-09-954-456-554
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Sequence 3, Appli
Sequence 93, Appl
Sequence 554, App
Sequence 30015, A
                                                                   Description
                                                                                                                                                    printed,
                           Alignment Scores: Pred. No.:
                                                                    ; NAME/KEY: CDS
; LOCATION: (1)..(1293)
US-10-075-846-3
                                                                                                                                                                                                                                                                                                                                                                  US-10-075-846-3
 Percent Similarity:
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; SEQ ID NO 3
FENGTH: 1640
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                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/10075846 Publication No. US20030032608A1 GENERAL INFORMATION:
                                                                                                                                                                           APPLICANT: Bristol Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL GLYCINE RECEPTOR ALPHA SUBUNI
TITLE OF INVENTION: IN THE GASTROINTESTINAL TRACT, HGRA4, and SPLICE VARIANT THER
FILE REFERENCE: DO079 NP
CURRENT APPLICATION NUMBER: US/10/075,846
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: US 60/269,535
PRIOR APPLICATION NUMBER: US 60/269,535
PRIOR STILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin version 3.0
                                                                                                          LENGTH: 1640
TYPE: DNA
ORGANISM: homo s
FEATURE:
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10 US-09-784-300-865
10 US-09-784-801-894
9 US-10-198-846-7241
9 US-10-198-846-7241
9 US-10-25-567A-343
9 US-09-764-891-8979
9 US-09-764-891-725
10 US-09-9880-197-3330
9 US-09-764-891-725
10 US-09-967-768A-314
10 US-09-967-768A-314
10 US-09-967-768A-314
10 US-09-967-768A-314
10 US-09-918-935-256
9 US-09-7880-192-375
10 US-09-918-936-256
9 US-09-918-936-256
9 US-09-918-936-256
9 US-09-918-936-256
9 US-09-918-91-1221
10 US-09-918-91-1221
10 US-09-918-91-1221
10 US-09-925-300-16
9 US-09-925-301-18
9 US-10-080-376-18
9 US-10-080-376-18
9 US-10-082-671-24
9 US-10-082-671-24
9 US-10-097-100-18
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             Length:
Matches:
 Conservative:
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Sequence 304, App Sequence 23458, A Sequence 23458, A Sequence 272, App Sequence 27, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 22, Appl Sequence 24, Appl Sequence 27, Appl Sequence 24,
1640 16 0

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US-09-954-456-554; Sequence 554, Application US/09954456; Patent NO. US20020115057Al; GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-93
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US-09-938-842A-93/c
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Query Match;
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                                        PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
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                                                                                                                                                                                                      APPLICANT: Young, Paul TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using TITLE OF INVENTION: Sets FILE REFERENCE: 689290-76 CURRENT APPLICATION NUMBER: US/09/954,456 CURRENT FILING DATE: 2001-09-18 CURRENT FILING DATE: 2001-09-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-06-22
NUMBER OF SECULO NUMBER: US 60/300,111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
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APPLICATION NUMBER: US/60/235,637 FILING DATE: 2000-09-26
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Matches:
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Best Local Similarity:
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PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
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OTHER INFORMATION: n=a
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                                                                                                                APPLICATION NUMBER: PCT/US01/00669 FILING DATE: 2001-01-30
                                                                                                                                                    APPLICATION NUMBER: PCT/US01/00664 FILING DATE: 2001-01-30
                                                                                                                                                                                         FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/236,359 FILING DATE: 2000-09-27 APPLICATION NUMBER: PCT/US01/00666
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                                  APPLICATION NUMBER: PCT/US01/00668 FILING DATE: 2001-01-30
                                                                                           APPLICATION NUMBER:
                  APPLICATION NUMBER: PCT/US01/00663
                                                                           FILING DATE: 2001-01-30
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FILING DATE:
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Hanzel, David K.
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2001-01-30
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FILING DATE:

2001-01-30

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Query Match:
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
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PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: Aeomica-X-1
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OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
OTHER INFORMATION: NT HIT: AB021490.2, EVALUE 7.40e-01
OTHER INFORMATION: EST_HUMAN HIT: BE612820.1, EVALUE 1.10e+00
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О.:
                                                                                                             APPLICATION NUMBER: PCT/US01/00666 FILING DATE: 2001-01-30
                                                                                                                                                           APPLICATION NUMBER: US 60/236,359 FILING DATE: 2000-09-27
                                                                   FILING DATE: 2001-01-30
                                                                                       APPLICATION NUMBER: PCT/US01/0066
                        FILING DATE:
                                           APPLICATION NUMBER: PCT/US01/00664
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Hanzel, David K.
NUMBER: PCT/US01/00669
                        2001-01-30
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Matches:
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; ORGANISM: Homo sapiens
; FEATURE:
; FEATURE:
; OTHER INFORMATION: MAP TO AL138761.3
; OTHER INFORMATION: EXPRESSED IN BRAIN,
; OTHER INFORMATION: EXPRESSED IN HELA,
; OTHER INFORMATION: EXPRESSED IN ADULT I
; OTHER INFORMATION: EXPRESSED IN FETAL I
US-09-864-761-13469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
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US-10-026-188-3
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                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

APPLICANT: Zuker, Charles S.

APPLICANT: Zhang, Yifeng

APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Assays for Taste Receptor Cell Spec:
TITLE OF INVENTION: Ion Channel
                                                                                                                              SOFTWARE: FastSEQ for Windows Version SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 13469
LENGTH: 597
TYPE: DNA
                                                       LENGTH: 249487
TYPE: DNA
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/10026188 Patent No. US20020164645A1
                                                                                                                                                                                                                                  FILE REFERENCE: 02307E-114910US
CURRENT APPLICATION NUMBER: US/10/026,188
CURRENT FILING DATE: 2001-12-21
                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/259,379
PRIOR FILING DATE: 2000-12-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 2001-01-29 NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: PCT/US01/00670 PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/US01/00661 PRIOR FILING DATE: 2001-01-30
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                OTHER INFORMATION: mouse genomic region containing ltrpc5
                                           FEATURE:
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52.00
92.31%
76.92%
69.33%
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IN HELA, SIGNAL = 1.6
IN ADULT LIVER, SIGNAL =
IN FETAL LIVER, SIGNAL =
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Alignment Scores:

2.25e+04

Length:

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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11273
LENGTH: 497
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OTHER INFORMATION: n equals
NAME/KEY: misc feature
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ORGANISM: Homo sapiens
                                                                                                       OTHER INFORMATION: n equals
                                                                                                                                                                                                              LOCATION: (389)
OTHER INFORMATION: n equals
                                        NAME/KEY: misc feature
                                                      OTHER INFORMATION: n equals
                                                                                       NAME/KEY: misc feature
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OTHER INFORMATION: n equals
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   INFORMATION: n equals
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80.00%
73.33%
65.33%
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                                                      a,t,g,
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Indels:
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Best Local Similarity:
Query Match:
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: OTHER INFORMATION: n equals a,t,g,
US-09-783-590-11273
                                                                                                                        US-09-974-300-865/c
                                                                                                                                            RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                     Sequence 865, Application US/09974300 Patent No. US20020146721A1 GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For
TITLE OF INVENTION: Expression
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OTHER INFORMATION: n equals
NAME/KEY: misc feature
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OTHER INFORMATION: n equals
NAME/KEY: misc feature
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OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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48.00
84.62%
69.23%
64.00%
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                  Monitoring Multiple Gene
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Conservative:
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APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, ANT
TITLE OF INVENTION: FOR LDENTIFICATION, ASSESSMENT, PRE
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TITLE OF INVENTION: THERAPY OF BREAST CANCER
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT APPLICATION NUMBER: 60/306,220
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR APPLICATION NUMBER: 60/306,220
SECO ID NO 12894
LENGTH: 720
TYPE: DNA
CTOANTEN: Homo santens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 865
LENGTH: 576
                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens

FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 1, 2, 3, 716, 717,

; OTHER INFORMATION: n = A,T,C

US-10-198-846-12894
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Best Local Similarity:
Query Match:
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Best Local Similarity:
                                                                                                                                                                                                                                         Alignment Scores
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RESULT 10
                                                                                                 US-10-075-846-4_COPY_192_207 (1-16) x US-10-198-846-12894 (1-720)
                                                                                                                                                                                                           Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12894, Application US/10198846 Publication No. US20030099974A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lillie, James APPLICANT: Xu, Yongyao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 576
TYPE: DNA.
ORGANISM: Bacillus licheniformis
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APPLICANT: LILIE, James
APPLICANT: Wang, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
APPLICANT: Westimann, Kathleen
ITITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, ANI
ITITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PRI
ITITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT APPLICATION NUMBER: 0007-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
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                                                                                                                                                                  SOFTWARE: Patent; SEQ ID NO 343; LENGTH: 5399; TYPE: DNA ORGANISM: Homo:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 343, Application US/10225567A - Publication No. US20030113798A1 GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences APPLICANT: Brown, Joseph P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7241
LENGTH: 791
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PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Datasto
                                                                                                                                                                                                                                                                                                                       APPLICANT: Burmer, Glenna C.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christeine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
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LOCATION: 282, 300, 554, 592,
OTHER INFORMATION: n = A,T,C c
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US-09-764-891-8979
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Publication No. US2003007780881
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or NUMBER OF SEQ ID NOS: 10231
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8976
LENGTH: 10468
TYPE: DNA
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8879
LENGTH: 10468
TYPE: DNA
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
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; LOCATION: (1)...(263)
; OTHER INFORMATION: n = A,T,C
US-09-918-995-30770
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CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 30770
LENGTH: 263
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Publication NO. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
                                                                                                                                                                                                                                                   SEQ ID NO 3940
LENGTH: 381
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                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/983,965 CURRENT FILING DATE: 2001-10-26 PRIOR APPLICATION NUMBER: US 09/465,231 PRIOR FILING DATE: 1999-12-15 PRIOR APPLICATION NUMBER: US 60/113,678 PRIOR APPLICATION NUMBER: US 60/113,678 PRIOR FILING DATE: 1998-12-17
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
APPLICANT: MATHIALAGAN, NAGAPPAN
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 37-21(10297)C
                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 5912
                                                                                                                                                                                            FEATURE:
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Command line parameters:

-MODEL-frame+_p2n.model -DEV=xlp
-O_-/cgn2_1/USPTO_spool_VS10075846/runat_25062003_163648_5157/app_query.fasta_1.782
-OB-EST -OFMT-fastap -SUFFIX-p2n.rst -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-bits -STARF-1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST-45
-DOCALIGN=200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL
-OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN-0 -MAXIEN-20000000
-USER-US10075846_eCGN_1_1_3724_erunat_2506203_163648_5157 -NCPU-6 -ICPU-3
-NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLOCK-100 -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPEXT-0.5 -FGAPOP-6
-PGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

	AUTHORS	REFERENCE			ORGANISM		SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AG076357/c	RESULT 1	
Totoki.Y., Watanabe,H. and Sakaki,Y.	Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,	1	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Pan troglodytes	BAC Library clone:PTB-070I15.F.	Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male	GSS.	AG076357.1 GI:16628159	AG076357 .	Ξ,	AG076357 795 bp DNA linear GSS 03-NOV-2001			

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TITLE
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BQ484167
BQ484167.1 GI:21328786
EST
Chicken.
                                                                               University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-6473
Fax: 302-831-2822
Email: ckeeler@udel.edu.
                                                                                                                                                                 Unpublished (2002)
Contact: Calvin Keeler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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Totoki, Y., Watanabe, H. and
Direct Submission
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            /organism="Gallus gallus"
/db_xref="taxon:9031"
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/clone="pmp1c.pk002.b9"
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Tissue Procurement: ATCC
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601556067F1 NIH_MGC_58 Homo
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Plate: LLCM492 row: f column:
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Cone distribution: MGC clone distribution information can
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/clone_lib="NIH_MGC_58"

/clone_lib="NIH_MGC_58"

/clone_type="hypernephroma"

/tissue_type="hypernephroma"

/tissue_type="hypernephroma
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/lab_host="E.coli XL-10 Blue"
/note="Vector: pBluescript II-SK"
119 c 56 g 60 t 1 others
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/sex="Male and Female"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
SerSerSerIleLeuCysSerProLeuProSerLeuSerLeuSer 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/ob_xref="taxon:9606"
/clone="IMAGE:4768033"
/clone="IMAGE:4768033"
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Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: dduun@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0313 row: I column: 12
Seg primer: CACACAGGAAACAGCTATGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
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1 (bases 1 to 128)
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                                                                                                                                                                                                                                                                  was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                  adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0313I12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="E. Coli strain XL10-Gold, T1-resistant, F
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="Male"
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1 (bases 1 to 263)

White,J.A., Todd,J., Newman,T., Focks,N., Girke,T., Martinez de Ilarduya,O., Jaworski,J.G., Ohlrogge,J. and Benning,C.
A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil Plant Physiol. 124 (4), 1582-1594 (2000)
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29621 Lambda-PRL2
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Fax: 517 353 9334
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/tissue_type="seed"
/dev_stage="5-13 days after flowering"
/lab_host="E.coli"
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/strain="Columbia"
/db_xref="taxon:3702"
/clone="600035219R1"
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Spermatophyta; Magnoliophyta; endicotyledons; Arabidopsis.
  Seki, M.,
                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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MSU-DOE Plant Research Laboratory
Michigan State University
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//Clone_lib="Lambda-PRL2"
//Other="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
//Inote="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
//Inote="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
//Inote="Vector: lambda Zip-Lox; Site_2: Not;
//Inote="Vector: lambda Zip-Lox; Sal; Site_2: Not;
//Inote="Vector: lambda Zip-Lox; Inot; Jambda Zip-Lox; Inot; Jambda Zip-Lox; Indicator: Inot; Jambda Zip-Lox; Inot; Inot; Jambda Zip-Lox; Inot; Inot; Jambda Zip-Lox; Inot; Inot; Jambda Zip-Lox; Inot; Inot; Jambda Zip-Lox; Inot;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oligo dT primed cDNA.
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/clone="196B17M4"
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details.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
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WHE1651-1654_A09_A09ZS Wheat heat stressed flag leaf cDNA library
Triticum aestivum cDNA clone WHE1651-1654_A09_A09, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
                                                                                                          1 (bases 1 to 470)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Har Anderson,O.D., Chao,S., Lazo,G.R., Malatrasi,M., Miller,R., P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Malatrasi,M., Miller,R., Ryuyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D. The structure and function of the expressed portion of the whee genomes - Heat stressed flag leaf cDNA library Unpublished (2000)
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3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
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Plant Functional Genomics Research Group
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and Shinozaki, K
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/lab_host="DH10B"
/note="Site_1: BamHI; Site_2: SalI; subjected to dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, hr) treatments"
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P., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.
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/db_xref="taxon:3702"
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1 (bases 1 to 547)
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AV548451 Arabidopsis
CDNA clone RZL54e05F
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                                                                                Yana 1532-3, Kisarazu, Chiba
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/dev_stage="Full tillering stage"
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/lab_host="E coli SOLR"
/lab_host="E coli SOLR"
/note="vector: Lambda Uni-ZAP XR, excised phagemid;
/note="vector: Lambda Uni-ZAP XR, excised phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give phagemids in the Uni-ZAP XR, excised to
asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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/organism="Arabidopsis thaliana"

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A large scale analysis of cDNA in Arabidopsis thaliana: Generation
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1: asamizu@kazusa.or.jp, URL:http://www.kazusa
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/tlssue_type="roots"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI;
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/strain="Columbia"
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/clone_lib="Arabidopsis thaliana
/tissue_type="roots"
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The First Laboratory for Plant (
Kazusa DNA: Research Institute
Yana 1532-3, Kisarazu, Chiba 29
Email: asamizu@kazusa.or.jp, UR
Location/Qualifiers
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Unpublished (1997)
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                                                                                                                                                         Cereal Research Centre, Agriculture and Agri-food Canada 195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-2340
Email: scloutierem.agr.ca
Email: scloutierem.agr.ca
primer were from the 5' end (same with forward primer and primer agr.ca).
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Contact: Shaying Zhao, William Nier
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2002)
Contact: Dr. Sylvie Cloutier
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/RPCI11 Human Male BAC Library"
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/db_xref="GDB:7567828"
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JOURNAL COMMENT
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VERSION
KEYWORDS
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BJ268516/c
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;

Triticeae; Triticum;

1 (bases 1 to 615)

Ogihara, Y. and Murai, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BJ268516 615 bp mRNA linear EST 09-APR-2002
BJ268516 Y. Ogihara unpublished cDNA library, Wh_oh Triticum
aestivum cDNA clone whoh17f17 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2002)
Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST
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                                                                                                                                                                                                                                                                                                                                                                                                                      Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Expressed genes in Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCAGCTCTTCTGCTGTAGCCCTCTCCCTGGTTTGAGCAGCAGCCTT
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/lab_host="E. coli DH10B"
/note="Vector: pCMV-SPORT5.0 (Invitrogen Technologies);
Site_1: NotI; Site_2: MluI; mRNA obtained from wheat se
of cultivar Glenlea 15 days post-anthesis"
a 126 c 183 g 106 t
/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site_1: EcoRI; Site_2: XhoI; Plants were grown under hydroponic conditions at UC Davis, salt stressed for 12 hours, and for 7 days, then dissected and frozen (Akhunov in J Dvorak Lab). Total RNA was prepared from sheath tissue, equal quantities of RNA were pooled from the two samples, polyA was purified from the pooled RNA, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab at the University of California, Riverside (Akhunov, Chin, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:4565"
/clone="TaE15015F10R"
/clone_lib="TaE15"
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/organism="Triticum aestivum"
                                                                                                                                                                                                                                            /clone_lib="Y. Ogihara unpublished cDNA library, Wh_oh"
/tissue_type="pistil at heading date"
/dev_stage="Feekes' scale 10.5"
                                                                                                                                                                                                                                                                                                            /organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="whoh17f17"
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Search completed: July 1, 2003, 00:55:32 Job time: 89.1163 secs

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

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Gapop 10.0 , Gapext 0.5
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SUMMARIES
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10	100400VBC	Result No. Score
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AAG42022	ABG16162	AAG24853	AAG24854	AAU16053	AAY37102	ABG04149	AAY54348 ·	AAO17460	AAB40561	AAY73448	AAU49188·	AAU46650	ABP05420	AAU33291	AA021708	AAY74114	AAG98446	AAU44557	AAM89167	AAU59452	ABP05968	AAU62995	AAU60466	AAM86900	AAB69150	AAW61532	ABB15852	AAE20147	AAM4 08 9 5	AAM39109	AAM39431	AAG00176	ABB17174	AAY14488
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ALIGNMENTS

RESULT 1

AAG38474 25 - FEB - 1999 05 - MAR - 1999 09 - MAR - 1999 23 - MAR - 1999 25 - MAR - 1999 29 - MAR - 1999 01 - APR - 1999 08 - APR - 1999 16 - APR - 1999 Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control; termination sequence. 18-OCT-2000 AAG38474; 25-FEB-2000; 06-SEP-2000 EP1033405-A2 Arabidopsis thaliana. Arabidopsis thaliana protein fragment SEQ ID NO: 47470. AAG38474 standard; Protein; 826 AA (first entry) 2000EP-0301439 99US-0121825 99US-012548 99US-0125788 99US-0125788 99US-0126785 99US-012785 99US-0127462 99US-0128234 99US-0128234 99US-0128714 99US-0128714 99US-0128715 promoter;

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RESULT 3
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Matches 11; Conservative
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73.3%;
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netic mapping; gene expression control;
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9-MAY-2000;
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    2000US-0216486.
2000US-021535.
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2000US-0229544.
2000US-0225778.
2000US-0225778.
2000US-0225758.
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2000US-0190076.
2000US-0198123.
2000US-0205515.
2000US-0209467.
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990S-0161993.
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; Pred. No. 20;
1; Mismatches
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17
17
                                                             Human; primer;
                                                                                                      Human protein sequence SEQ ID NO:19021.
                                                                                                                                                   26-JUN-2001
                                                                                                                                                                                            AAB95892;
                                                                                                                                                                                                                                  AAB95892 standard; Protein; 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-DEC
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                                                                                                                                                                                                                                                                                                                                                                      1 SSSILCSPLPSLSLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                               SSSCLVSPLPSLFLA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 3412; 1297pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barash
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0251989.
2000US-0251990.
2000US-0254097.
                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0251479.
2000US-0251856.
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                                                          detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.7%;
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                                                                                                                                                                                                                                                                                                                                                                                      15
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 47; DB Pred. No. 3.5; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
3.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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RESULT 6 ABB92207

ABB92207

standard; Protein;

490

Herbicidal; plant; agriculture; herbicide Herbicidally active polypeptide SEQ

ID NO 1418

31-MAY-2002

(first entry)

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TOKLLCSPLPHLAVS

69 15

SSSILCSPLPSLSLS

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Query Match
Best Local S
Matches 8
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                              the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
                                                                                                                                                                                                                                                                                  sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                     to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0ta
                                                                           Sequence
                                                                                                           of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                 complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                 of an oligonucleotide comprising a sequence complementary to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP1074617-A2
                                                                                                                                 represent oligonucleotides,
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Similarity
8; Conserv
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Sugiyama T, Wakamatsı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID 19021;
                                                                           160 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
   Conservative
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                 62.7%;
53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wakamatsu
                                                                                                                                   all of which are used in
Score 47; DB Pred. No. 7; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashi K, S
A, Nagai K,
                                     DB
                                     22;
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, Otsuki T;
                                     Length 160;
   Indels
                                                                                                                                   the exemplification
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Gaps
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Best Local S
Matches 11
WPI; 2001-639362/73
N-PSDB; AAS88177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypoptides or nucleic acids encoding them
                                    Drmanac RT,
                                                                                                                       30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200210210-A2
                                                                                   31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tietjen K, Weidler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-AUG-2001; 2001WO-EP09892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-FEB-2002
                                                            (HYSE-) HYSEQ INC
                                                                                                                                                                        WO200175067-A2
                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy;
food supplement; medical imaging; diagnostic; genetic (
                                                                                                                                                                                                                                                            Novel human
                                                                                                                                                                                                                                                                                    18-FEB-2002
                                                                                                                                                                                                                                                                                                              ABG23990;
                                                                                                                                                                                                                                                                                                                                    ABG23990 standard; Protein; 67 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-269010/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FARB ) BAYER AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-AUG-2001; 2001WO-EP09892
                                                                                                                                                 11-OCT-2001
                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                   210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 1418;
                                                                                                                                                                                                                                                                                                                                                                                                                       SSSILCSPLPSLSLSV 16
                                                                                                                                                                                                                                                                                                                                                                                                 SSSLLSSPLPPPSLPV 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  490
                                                                                                                                                                                                                                                            diagnostic protein #23981.
                                    Liu C,
                                                                                   2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.3%;
                                  Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 46;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23;
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RESULT 8
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XX NOVE
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Matches 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fire hypolitypublished_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide (II) sequences. (I) is useful as nypridisation processes polymerase chain reaction (PCR) primers, oligomers, and for chromosome polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant and the contract of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                      WPI; 2001-639362/73
                                                                                                                                                   Drmanac
                                                                                                                                                                                                                                                                                                      31-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; chromosome food supplement; m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human diagnostic protein #11053.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG11062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG11062 standard;
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                                                                                                                                                                                                             (HYSE-)
                                                                                                                                                                                                                                                                          23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SSSILCSPLPSLSL 14
                                                                                                                                                   RT,
                                                         AAS75249.
                                                                                                                                                                                                             HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                Liu C,
                                                                                                                                                                                                                                                                          2000US-0540217.
2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mapping; gene mapping; gene therapy; forensionedical imaging; diagnostic; genetic disorder
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                                                                                                                                             Tang
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78.6%;
                                                                                                                                                   ΥŢ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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New isolated polynucleotide and encoded polypeptides, useful

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RESULT 9
AAM23635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II) The CC polymucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or Guntitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC The polypeptide and polymucleotide sequences have applications in CC responsible for genetic disorders or other traits to assess biodiversity and or produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                25-JAN-2000;
17-JUL-2000;
03-AUG-2000;
15-SEP-2000;
                                       Tang
                                                                                                                                                                                                                                                                                     tomato; monkey; dog; sea urchin; diagnostics; forensic test; gene biodiversity; gene therapy; nutr:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess blodiversity -
                                                                                                                                                                       25-JAN-2001; 2001WO-US02687
                                                                                                                                                                                                      02-AUG-2001.
                                                                                                                                                                                                                                 WO200154477-A2
                                                                                                                                                                                                                                                             Human herpesvirus
                                                                                                                                                                                                                                                                                                                                 Human; sheep; plg; cow; fruit fly; yeast; hamster; macaque; horse;
                                                                                                                                                                                                                                                                                                                                                                   HHV-2
                                                                                                                                                                                                                                                                                                                                                                                              12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM23635 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide (II) sequences. (I) is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                    (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Toca r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences.
                                       YT,
                                                                                                                                                                                                                                                                                                                                                                 EST encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SSSILCSPLPSLSL 14
                        , Liu C, Z
Drmanac RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSSFLCSPLP-LSL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID No 41421; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89
                                                                                                2000US-0491404.
2000US-0617746.
2000US-0631451.
2000US-0663870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    relates to isolated polynucleotide (I) and II) sequences. (I) is useful as hybridisation probes,
                                       Zhou
                                                                                                                                                                                                                                                                                                                                                                protein SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60.7%;
78.6%;
                         Zhang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .68;
                        'n
                                      Qian XB,
                                                                                                                                                                                                                                                                                       chin; expressed sequence tag; to
gene mapping; genetic disorder;
nutrition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ۲.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 45.5;
Pred. No. 6.
                                                                                                                                                                                                                                                                                                                                                                ID NO: 1160
                           Werhman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                           wang
man T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
                                       2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                       Asundi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
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from WIPO
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RESULT 10
AAU14387
ID AAU14
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cow, pig, hamster, monkey, macaque, yeast, urchin and tomato. These were derived from from the organism of interest. They can be forensics, gene mapping, identification of biodiversity and for nutritional purposes. protein of the invention.
                                                                                                                                                                                                                                   Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviantibacterial; antiallergic; dermatological; haemostatic; antiasthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess
                                                           The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU14387 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated po
antibodies
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molecular weight markers,
            proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the abberrant protein expression or activity. The polypeptides can be used as
                                                                                                          Example 4;
                                                                                                                                                                                                                                                                                                                                                            02-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                           WO200155437-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue regeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human novel protein #258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                       Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage -
                                                                                                                                                                                                                                                                                                 25-JAN-2000; 2000US-0491404
                                                                                                                                                                                                                                                                                                                              25-JAN-2001; 2001WO-US02623
                                                                                                                                                                                                                                                                (HYSE-) HYSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention provides the protein
                                                                                                                                                                                                                                   YT,
                                                                                                                                                                                                     2001-451939/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20; Page 850-851; 1275pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
8; Conserv
                                                                                                                                                                                      AAS22692.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LCPPLPSLSCAI 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LCSPLPSLSLSV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide for treatment of diseases, diagnostics, raising
                                                                                                                                                                                                                                   Liu
                                                                                                         Page 795-796; 894pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; Antianaemic; osteopathic; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                  Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunogen; antibody; gene therapy; neurological disorder;
isease; inflammatory disorder; cancer; asthma; osteoporosi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         immune disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45;
Pred. No.
                                                                                                         English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DВ
15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and coding sequences of novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiviral;
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food

supplements,

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RESULT 11
AAY14488
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Best Local S
Matches 8
                                                                   Florence K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorders, stem cell disorders, regenerating bone, cartilage, tendon, ligament and/or nerve tissue, wound healing, treating burns, promoting the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis, anaemia, alzhelmer's, Parkinson's and Huntington's diseases, amylotrophic lateral sclerosis, stroke, immune deficiencies resulting from bacterial, viral or fungal infection or from autoimmunity, cancer, allergy, asthma, graft-versus-host diseases, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection. The present sequence represents a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptides. Polynucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to take the true to a tumour, in assays to determine biological activity, the true of the first true of tumour, in assays to determine biological activity, the true of the first true of the first true of tumour, in assays to determine biological activity, the true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first true of the first t
                    WPI; 1999-277587/23
                                                                                                                                                                                                                                                                                                                                                                                                     08-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cognitive disorder; schizophrenia; prostate; obesity; osteoclosteoporosis; arthritis; testis; lung; thyroiditis; thyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             raise antibodies/elicit an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands. Polypeptides of the invention may also be useful in treating platelet
                                                                                                               Brewer LA,
                                                                                                                                                                                                                                               09-OCT-1997;
09-OCT-1997;
                                                                                                                                                                                                                                                                                                09-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                 09-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   endocrine; metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fragment of human secreted protein encoded by gene 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY14488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                      HUMA-) HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptides are used to identify compounds which bind to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143
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8; Conser
                                                                                          ΚA,
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                                                                                          Duan R,
Greene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                      GENOME
                                                                                                                                                                                                                  97US-0071498.
97US-0061463.
97US-0061527.
97US-0061529.
97US-0061532.
97US-0061536.
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                                                                                                                  Ebner
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                                                                                                                                                                      SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .08;
                                                                                          Olsen
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Pred:
                                                                                                               Ferrie AM,
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                                                                                             ,SH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                malabsorption;
                                                                                             Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
15;
                                                                                                               Florence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
                                                                                          Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gastritis; neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  osteoclast; thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        digestion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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RESULT 12
ABB17174
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30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                          31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
antiparasitic; cardiant; immune disorder; cardiovascular disorder;
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antiparkinsonian; antisickling; antianaemic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
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19-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JAN-2002
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                 2000US-0215135.
2000US-0216647.
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2000US-0218290.
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2000US-0225266. 2000US-0225267. 2000US-0225268. 2000US-0225270. 2000US-0225270. 2000US-0225757. 2000US-0220964. 2000US-0224518. 2000US-0224519. 2000US-0225213.

2000US-0225758. 2000US-0225759. 2000US-0226279.

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17-NOV-2000;
The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                             cancers
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N-PSDB; ABA13500.
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2000US-0231968. 2000US-0232397. 2000US-0232398. 2000US-0229509. 2000US-0229513. 2000US-0230437. 2000US-0230438. 2000US-0231443. 2000US-0231244. 2000US-0231244. 2000US-0231244.

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                                                                                                                                 The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' conds and any thorefore by used to be a full location of the sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epilepsy; and (f) infectious diseases such as viral, bacteria and parasitic infections.

Note: The sequence data for this patent did not form part of printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                        Sequence
                                                                              DNAs. 5' ESTs are also used in diagnostic, forensic, gene theraperchromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                      ends and can therefore be used to obtain full length cDNAs and genomic
                                                                                                                                                                                                                                                                          Claim 13;
                                                                                                                                                                                                                                                                                                                                                                                               Dumas Milne Edwards
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                                                                                                                                                                                                                                                                                                   diagnostic,
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69.2%;
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RESULT 14
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25-APR-2000;
09-JUL-2000;
                                                        Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                   in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as
                                                                                                                                                                                 The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful
                                                                                                                                                                                                                                                                                                                                              Tang
Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; dryg screening; arthritis; inflammation;
Sequence
                                    C.N.S disorders
Note: The seque
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29-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; nootropic; immunosuppressant; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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QA,
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Wang Z,
Zhou P,
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                                    sequence data
                                                                                                                                                                                                                                    SEQ ID
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2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
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2000US-0693036
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 AA;
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Wehrman T, X
Goodrich R,
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                                                                                                                                                                                                                                                         polypeptides, useful system injuries -
                                     for this
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Xu C, Xue AJ,
R, Drmanac RT;
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                                    patent did
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Yang
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                                     form
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                                     of.
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                                    the printed
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Query Match

58

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Score

44;

DB 22;

Length 887;

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RESULT 15
AAM39109
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25-APR-2000; 2000US-0552317;
09-JUL-2000; 2000US-0598042;
19-JUL-2000; 2000US-0620312;
03-AUG-2000; 2000US-0653450;
14-SEP-2000; 2000US-0653191;
19-CCT-2000; 2000US-0693036;
                                                               The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
                                                                                                                                                                                                                                                                                                                                                                                           Tang YT,
Wang J,
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; cNS; peripheral nervous system; cNS; Alzheimer's; Parkinson's disease; hantington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                  Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                WPI; 2001-442253/47.
N-PSDB; AAI58265.
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                                                                                                                                                                                                                                                                     Example 4; SEQ ID NO 2254; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JUL-2001.
            specification
                                       assays for receptor activity, arthritis and inflammation, C.N.S disorders.
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                       The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                           , Liu C,
Wang Z,
Zhou P,
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SSQIITSPLPSVS 454
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Wehrman T, X
Goodrich R,
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Xu C, Xue AJ,
Drmanac RT;
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Yang Y,
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Zhang J;
                                                       leukaemias and
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CNS;
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145 SPSILQCPLPSLSL 158
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        1 SSSILCSPLPSLSL 14
                                                               274 AA;
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                                        57.38;
71.48;
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                                 Mismatches
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Search completed: June 25, 2003, 17:15:33 Job time: 3.32662 secs

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2: /cgn2_6/ptodata/1
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  262574 seqs, 29422922 residues
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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US-09-178-18-19-13
PCT-US95-11114-13
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US-09-288-143-205
                                                               RESULT 2
US-09-177-249-208
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Best Local S
Matches 8
Sequence 208, Application US/09177249
Patent No. 6229064
GENERRAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Ohad, NIT
APPLICANT: Kiyosue, Tomobiro
APPLICANT: Kyosue, Tamin
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36 48.0 896 4 US-08-618-957A-10 36 48.0 898 2 US-08-618-957A-10 36 48.0 898 4 US-08-618-957A-10 36 48.0 906 2 US-08-618-957A-9 36 48.0 906 2 US-08-618-957A-9 36 48.0 906 2 US-08-618-957A-9 36 48.0 908 2 US-08-618-957A-9 36 48.0 908 2 US-08-640-389A-8 36 48.0 958 2 US-08-640-389A-8 36 48.0 958 4 US-08-58-18-957A-8 36 48.0 950 1 US-08-58-190-3 36 48.0 960 2 US-08-693-697-8 36 48.0 960 2 US-08-693-697-8 36 48.0 960 3 US-08-693-695-8 36 48.0 960 3 US-08-693-695-8 36 48.0 960 3 US-08-618-957A-3 36 48.0 960 3 US-08-618-957A-3 36 48.0 960 3 US-08-618-957A-3 36 48.0 960 3 US-08-618-957A-3 36 48.0 960 3 US-08-693-695-8
896 4 US-08 898 2 US-08 906 2 US-08 908 2 US-08 908 2 US-08 908 2 US-08 958 2 US-08 950 1 US-08 960 2 US-08 960 2 US-08 960 2 US-08 960 2 US-08 960 2 US-08 960 2 US-08
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80 - 50 80

ALIGNMENTS

FILE REFERCE: PZ018P1 FILE REFERCE: PZ018P1 CURRENT APPLICATION NUMBER: US/09/288,143 CURRENT FILING DATE: 1999-04-08 EARLIER APPLICATION NUMBER: 60/061,463 EARLIER APPLICATION NUMBER: 60/061,463 EARLIER APPLICATION NUMBER: 60/061,529 EARLIER APPLICATION NUMBER: 60/071,498 EARLIER APPLICATION NUMBER: 60/071,498 EARLIER APPLICATION NUMBER: 60/061,527 EARLIER APPLICATION NUMBER: 60/061,527 EARLIER APPLICATION NUMBER: 60/061,527 EARLIER APPLICATION NUMBER: 60/061,536 EARLIER APPLICATION NUMBER: 60/061,536 EARLIER APPLICATION NUMBER: 60/061,536 EARLIER FILING DATE: 1997-10-09 EARLIER APPLICATION NUMBER: 60/061,532 EARLIER FILING DATE: 1997-10-09 EARLIER PILING DATE: 1997 GENERAL INFORMATION: APPLICANT: Brewer et Sequence 205, Application US/09288143 Patent No. 6433139 TITLE OF INVENTION: 53 Human Secreted Proteins FILE REFERENCE: PZ018P1 Local Similarity les 8; Conserv 2 SSILCSPLPSLS 13 :| ||||:||: 15 TSQLCSPMPSLN 26 Conservative 58.7%; 66.7%; Score 44; Pred. No. Mismatches DB 4; 1; Length 75; Indels

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PPLICANT: Margossian, Linda

PPLICANT: Harada, John

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Query Match
Best Local Similarity
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NUMBER OF SEQ ID NOS: 324
SOFTWARE: PATENTIN VEr. 2.0
SEQ ID NO 208
LENGTH: 106
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CURRENT FILING DATE: 1998-10-22
EARLIER APPLICATION NUMBER: US 09/071,838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: The Regents of the University of California TITLE OF INVENTION: NUCLEIC ACIDS THAT CONTROL Seed an TITLE OF INVENTION: Development in Plants FILE REFERENCE: 023070-086120US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPLICANT:
                                                    NFORMATION FOR SEQ ID NO: 2:
                                                                                   NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: M0656/7036
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/051,753
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows
CURRENT APPLICATION DATA:
                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/0
FILING DATE: 12-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Baltimore, David
TITLE OF INVENTION: DAXX, A NOVEL FAS-BINDING
TITLE OF INVENTION: PROTEIN THAT ACTIVATES JNK AND APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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 TYPE: a
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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: 739 amino acids amino acid
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Khosravi-Far,
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72.78;
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Pred. No. 7
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                                                                         : NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No. 6287786 1772859CD1
US-09-629-774A-2
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                                                                                                                                : SOFTWARE: PERL Program
: SEQ ID NO 2
: LENGTH: 291
: TYPE: PRT
: ORGANISM: Homo sapiens
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SEQ ID NO 2
LENGTH: 291
TYPE: PRT
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                        APPLICANT: Kaser, Matthew R.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: PHOSPHOLIPID TRANSFER PROTEIN
FILE REFERENCE: PC-0003-1 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/328,869B
CURRENT FILING DATE: 1999-06-08
NUMBER OF SEQ ID NOS: 17
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APPLICANT: Baughn, Marilah, R.
TITLE OF INVENTION: PHOSPHOLIPID TRANSFER PROTEIN
FILE REFERENCE: PC-0003 US
                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/629,774A
CURRENT FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 17
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                                                                                                                     FEATURE:
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FRAGMENT TYPE:
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TOPOLOGY: lin
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5; 6287786
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                             Score 39; DE Pred. No. 95;
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Pred. No.
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Pred. No.
                 Mismatches
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US-08-299-187-13
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PCT-US95-11114-13
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INFORMATION FOR SEO ID NO: 13
SEQUENCE CHARACTERISTICS:
"FNGTH: 13 amino acids
"FNGTH: 13 arid
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                                                      Sequence 13, Application PC/TUS95111114 GENERAL INFORMATION:
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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APPLICANT: Ricketts, Michael H.
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                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 601
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              Manowitz, Paul
Poretz, Ronald D.
Park, David
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 Ricketts, Michael H.
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Pred. No. 4.6;
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US-07-956-700B-84
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                                                                                                                                                    Sequence 84, Application US/07956700B Patent No. 5539092
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                                                                                                                          GENERAL INFORMATION: APPLICANT: Robert
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                                                                                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Home
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                        TITLE OF INVENTION: Cy
TITLE OF INVENTION: Ca
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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NAME: Jackson Esq., Davi
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CORRESPONDENCE ADDRESS:
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REFERENCE/DOCKET NUMBER: 115
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CLASSIFICATION:
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STATE: New Jerse
                           ADDRESSEE: Arnold, White & Durkee STREET: 321 No. 5539092th Clark Street
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CLASSIFICATION:
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FILING DATE: 21-JUN-1995
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Chicago
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411 Hackensack Avenue
                                                                                                       Robert Haselkorn and Piotr Gornicki
VENTION: Cyanobacterial and Plant Acetyl-Coa
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

Floppy Disk

COUNTRY:

60610

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Query Match
Best Local Similarity
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US-08-476-537-84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 5756290
                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/956,700
FILING DATE: 10/21/92
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. No. 5756290thrup
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD:058
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                TELEFAX: 1-312-
INFORMATION FOR SEQ
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                                                                                                                                                                                                                                                                                                                                                     STREET: Jac.
CITY: Chicago
CITY: Illinois
THATE: IISA
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                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: CY
TITLE OF INVENTION: CA
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. No. 5539092thrup
REGISTRATION NUMBER: 33,268
                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC CON
OPERATING SYSTEM: PC
SOFTWARE: ASCII-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: U: FILING DATE: 19921002 CLASSIFICATION: 800
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                TELEPHONE:
                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                            SOFTWARE: ASCII-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: ARCD: 058
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X: 1-312-755-4489
N FOR SEQ ID NO: CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                   E: Arnold, White & Durkee
321 No. 5756290th Clark Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08476537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Robert Haselkorn and Piotr Gornicki
RVENTION: Cyanobacterial and Plant Acetyl-Coa
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1-312-755-4489
1-30 TD NO: 84:
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SYSTEM: PC-DOS/MS-DOS
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                                               1-312-744-0090
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RESULT 11 US-08-475-879-84

; Sequence 84, Application US/08475879; ; Patent No. 5972644

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; STRANDEDNESS:
; TOPOLOGY: Lin
; MOLECULE TYPE:
US-08-476-537-84
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Best Local Similarity
Thes 7; Conserve
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                                                     Matches
                                                                               Query Match
                                                                   Best
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APPLICANT: Robert
                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/956,700
FILING DATE: 10/21/92
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. No. 5792627thrup
REGISTRATION NUMBER: 33,268
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 1-312-744-0090
                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Chicago
                                                  Local Similarity hes 7; Conserv
                                                                                                                                    STRANDEDNESS: Sir
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/01 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 251 um
                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: ASCII-DOS
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                                                                                                                                                                           LENGTH:
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181 TSSVLRSPMPGVVVAV 196
                          1 SSSILCSPLPSLSLSV 16
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                                                                                                                                                             Amino acids
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321 No. 5792627th Clark Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                       1-312-755-4489
                                                     Conservative
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ENTION: Cyanobacterial and Plant Acetyl-Coa
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                                                                                                                       Peptide
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43.8%;
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Pred. No. 1.1e+02;
                                                                  Score 38;
Pred. No.
                                                     Mismatches
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                                                                  1.1e+02;
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                                                    Indels
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                                                    Gaps
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Patent No. 5972644 5786170

GENERAL INFORMATION:

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                                                                    SEQ ID NO 84
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                    sequence 84, Application US/09433043B
Patent No. 6399342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 50.7%; Score 38; 18est Local Similarity 43.8%; Pred. No. 1 Matches 7; Conservative 6; Mismatch
                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                            FILE REFERENCE: ARCD:338US
CURRENT APPLICATION NUMBER: US/09/433,043B
CURRENT FILING DATE: 1999-10-25
                                                                                                                                                                                                                                                              APPLICANT: HASELKORN, ROBERT
APPLICANT: GORNICKI, PIOTR
TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-COA CARBOXYLASE
                                                                                                       NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn Ve
                                                                                                                                           PRIOR APPLICATION NUMBER: 07/956,700 PRIOR FILING DATE: 1992-10-02
                                                                                                                                                                              PRIOR APPLICATION NUMBER: 08/475,879 PRIOR FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 1-312-755-44
                                  ORGANISM: Artificial Sequence
                                                       TYPE: PRT
OTHER INFORMATION: Description of Artificial Sequence:
                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 07/956,700
FILING DATE: 10/21/92
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. No. 5972644 5786170thrup
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD:058
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: Amino acids
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STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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                                                                                                        PatentIn Ver.
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321 No. 5972644 5786170th Clark Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :SS: Single
Linear
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)N: 536
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1.1e+02;
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Best Local Similarity
Thes 7; Conserve
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                                                                                            ; MOLECULE TYPE: protein US-08-476-008-50
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                      Query Match
Best Local Similarity
7; Conser
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                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/476,008
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,063
FILING DATE: 13-SEP-1994
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/576,537
ENTING DATE: 31-NUG-1060/576,537
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                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., MonsaisTREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 30. REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 0 FILING DATE: 31-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                           TOPOLOGY: linear
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1 SSSILCSPLPSLSLS 15
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                                                                                                                                                                                                        (314)537-6047
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                              50.7%; Score 38; DB 1; llarity 46.7%; Pred. No. 2.2e+02; Conservative 5; Mismatches 3
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monsanto Co. BB4F
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                                                            Length 460;
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14 SSNVICAPPGSKSIS 28

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Sequence 50, App...
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Best Local :
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APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
                                                                                                                      GENERAL INFORMATION:
APPLICANT: Stalling:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEO ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 460 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION.
PRIOR APPLICATION DATA:
US 07/576,537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATION OPERATING SYSTEM: PC-DC SOFTWARE: Patentin Relaction DATA:
                                                                        APPLICANT:
                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 28-AUG-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: 6lyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 70
                                                                                                                                                                                                                                                                                                                  Local Similarity 46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10660)A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 31-AUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/306,063 FILING DATE: 13-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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         Barry, Gerard F.
Kishore, Ganesh M.
Kishore, Stephen'R.
Padgette, Stephen'R.
Stallings, William C.
Stallings, William C.
VVENTION: Glyphosate Tolerant
VVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
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700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (314)537-6047
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US-08-833-485-50

LED NO:

LOCTERISTICS:

460 amino acids

amino acids

TOPOLOGY: linear

MOLECULE TYPE: profile

US-08-833-485-50
Search completed: June 25, 2003, 17:18:07 Job time: 1.85906 secs
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                                                                                                          Query Match
Best Local Similarity
Trhas 7; Conserv
                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: IFILING DATE: 13-SEP-CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 0' FILING DATE: 31-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                           14 SSNVICAPPGSKSIS 28
                                                                                        SSSILCSPLPSLSLS 15
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                                                                                                                                                                                                                                                                                            : (314)737-6099
(314)737-6047
                                                                                                                        Conservative
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                                                                                                                        5
                                                                                                                                      Score 38;
Pred. No. 2
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                                                                                                                        Mismatches
                                                                                                                                                     DB 1;
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Minimum DB seq
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Perfect score:
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     US-10-075-846-4_COPY_192_207
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l: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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3: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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Listing first 45 summaries
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    508
756
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 US-10-075-846-74
US-10-075-846-15
US-10-075-846-15
US-10-075-846-15
US-09-764-891-3412
US-09-771-161A-102
US-09-771-161A-192
US-09-771-161A-193
US-09-771-161A-193
US-09-771-161A-193
US-09-771-1838-208
US-09-711-838-208
US-09-711-838-208
US-09-747-155-49
US-10-150-821-4
US-09-747-155-49
US-09-746-284-23
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US-09-746-284-23
US-09-746-284-23
US-09-966-871-86
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1307.255 Million cell updates/sec
Sequence 74, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 205, App
Sequence 102, App
Sequence 101, App
Sequence 193, App
Sequence 208, App
Sequence 208, App
Sequence 4, Appli
Sequence 4, Appli
Sequence 29, App
Sequence 23, Appli
Sequence 23, Appl
Sequence 23, Appl
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Sequence 86, Appl
Sequence 86, Appl
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US-10-075-846-74
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Best Local S
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	115-10-174-590-549	US-09-740-668A-42	US-10-256-702-7	US-09-933-261-7	US-10-138-927-45	US-10-101-464A-915	US-09-816-127-1	US-09-733-300-4	US-09-965-529-12	US-09-861-696-50	US-09-464-099A-50	US-09-796-753-142	US-10-085-108-22	US-09-864-761-37903	US-09-739-907-157	US-10-106-698-5785	US-09-864-761-47002	US-09-864-761-36023	US-10-205-823-60	US-10-106-698-4697	US-09-925-301-985	US-09-841-132-404	US-09-764-891-3995	US-09-811-284-256	US-09-764-891-2743	US-10-106-698-5490
pequence sao, app	л	Sequence 42, Appl		Sequence 7, Appli	Sequence 45, Appl	Sequence 915, App	Sequence 1, Appli	Sequence 4, Appli	Sequence 12, Appl	Sequence 50, Appl	Sequence 50, Appl	Sequence 142, App	Sequence 22, Appl	Sequence 37903, A	Sequence 157, App	Sequence 5785, Ap	Sequence 47002, A	Sequence 36023, A	Sequence 60, Appl	Sequence 4697, Ap	Sequence 985, App	Sequence 404, App	Sequence 3995, Ap	Sequence 256, App	Sequence 2743, Ap	Sequence 5490, Ap

ALIGNMENTS

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RESULT 2
US-10-075-846-15
; Sequence 15, Application US/10075846
; Publication No. US20030032608A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL GLYCINE RECEPTOR ALPHA SUBUNI
; TITLE OF INVENTION: IN THE GASTROINTESTINAL TRACT, HGRA4, and SPLICE VARIANT THER
; FILE REFERENCE: D0079 NP
; CURRENT APPLICATION NUMBER: US/10/075,846
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: US 60/269,535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-075-846-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/075,846
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: US 60/269,535
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin version 3.0
SEQ ID NO 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 74, Application US/10075846 Publication No. US20030032608A1 GENERAL INFORMATION:
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TITLE OF INVENTION: POLYNUCLECTIDES ENCODING A NOVEL GLYCINE RECEPTOR ALPHA SUBUNI
TITLE OF INVENTION: IN THE GASTROINTESTINAL TRACT, HGRA4, and SPLICE VARIANT THER
FILE REFERENCE: D0079 NP
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11 Similarity 100.0%;
16; Conservation
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Pred. No.
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; NAME/KEY: SITE ; LOCATION: (51) ; LOCATION: (51) ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-891-3412
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; SEQ ID NO 4
; LENGTH: 431
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-075-846-4
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                                                                                                                                                                                          Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3412
LENGTH: 83
     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                           Sequence 3412, Application US/09764891 Publication No. US20030077808A1 GENERAL INFORMATION:
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Best Local Similarity
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LENGTH: 312.
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Best Local Similarity
                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                         APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/075,846
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: US 60/269,535
PRIOR FILING DATE: 2001-02-16
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NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin version 3.0
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TITLE OF INVENTION: POLYMUCLECTIDES ENCODING A NOVEL GLYCINE RECEPTOR ALPHA SUBUNIT :
TITLE OF INVENTION: IN THE GASTROINTESTINAL TRACT, HGRA4, and SPLICE VARIANT THEREO;
FILE REFERENCE: D0079 NP
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                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                               TYPE: PRT
                                                                                                                                          FEATURE:
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192 SSSILCSPLPSLSLSV 207
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100.0%; Pred. No.
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     47;
DB 3;
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Query Match
Best Local Similarity
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; ORGANISM: Homo sapiens
US-10-150-111-205
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; ORGANISM: Homo sapiens
US-09-771-161A-102
                                                                      SOFTWARE: PatentIn version 3.0 SEQ ID NO 102
                                                                                                                                                                                                                                                                                                                                                          Sequence 102, Application US/09771161A Patent No. US20020110811A1
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LENGTH: 75
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APPLICANT: LEVINE, et al
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                                                                                                         PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
                                                                                                                                                                  PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES FILE REFERENCE: 802620-2005.1
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PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/061,463
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/061,529
PRIOR FILING DATE: 1997-10-09
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CURRENT FILING DATE: 2002-05-20
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                                         TYPE: PRI
                                                        LENGTH:
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b. US20030078386A1
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Pred. No. 7
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; SOFTWARE: PatentIn version 3.0; SEQ ID NO 192; LENGTH: 887; TYPE: PRT; ORGANISM: Homo saplens US-09-771-161A-192
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US-09-771-161A-101
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CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 13676
PRIOR APPLICATION NUMBER: 136619
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
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US-09-771-161A-192
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PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
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APPLICANT: LEVINE, et al.

TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES

FILE REFERENCE: 802620-2005.1

CURRENT APPLICATION NUMBER: US/09/771,161A

CURRENT FILING DATE: 2001-01-26

CURRENT FILING
                                                         Query Match
Best Local S
Matches 9
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APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
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LENGTH: 756
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Best Local
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Local Similarity 69.2%;
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69.2%;
                                                       Score 44; DB:
Pred. No. 94;
2; Mismatches
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Pred. No. 54;
2; Mismatches
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US-09-771-161A-193
; Sequence 193, Application US
; Patent No. US20020110811A1
; GENERAL INFORMATION:
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                                                                                                                                                   ; ORGANISM: Arabidopsis US-10-213-512-208
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US-10-213-512-208
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SEQ ID NO 193
LENGTH: 887
                                                                        Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 208
LENGTH: 106
TYPE: PRT
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Best Local Similarity 69.2%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 208, Appropriate Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                 APPLICANT: Goldberg, Robert B.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and
TITLE OF INVENTION: Fruit Development in Plants
FILE REFERENCE: 023070-086110US
CURRENT APPLICATION NUMBER: US/10/213,512
CURRENT APPLICATION NUMBER: US/20777,206
PRIOR APPLICATION NUMBER: US/09/177,206
PRIOR FILING DATE: 1998-10-22
PRIOR FILING DATE: 1998-10-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 13676
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES FILE REFERENCE: 80262-2005.1 CURRENT APPLICATION NUMBER: US/09/771,161A CURRENT FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 324
                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 09/071,838 PRIOR FILING DATE: 1998-05-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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61 MLCSPFPSLHL 71
                   4 ILCSPLPSLSL 14
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o. US20030110536A1
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                                                                        Conservative
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                                                                                          57.38;
72.78;
                                                                                          Score 43; DB Pred. No. 16;
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Pred. No.
                                                                          Mismatches
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Indels

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Length 106;

Indels

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JS-09-071-838-208

SENERAL INFORMATION:

tent No. US20020152501A1

Application US/09071838

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Query Match
Best Local Similarity
"atches 8; Conserv?
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US-10-150-821-4
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                            Sequence 4, Application US/10150821
publication No. US20020192758A1
GENERAL INFORMATION:
APPLICANT: Welcher, Amdrew A.
APPLICANT: Elliott, Gary S.
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 01017/37592
CURRENT APPLICATION NUMBER: US/10/150,821
CURRENT FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: US/9/911,842
PRIOR FILING DATE: 2001-07-24
PRIOR FILING DATE: 2001-07-24
   PRIOR
                  PRIOR
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TITLE OF INVENTION: 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: BASTLAN, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION: NAME: Bastian, Kevin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
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TOPOLOGY: linear
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 APPLICATION FILING DATE:
                                                                                                                                                                                                                                                                                                               61 MLCSPFPSLHL 71
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California
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Yadegari, Ramin
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ON: 800
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NUMBER: US 60/222,438: 2000-08-01
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72.7%;
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LENGTH: 216

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NAME/KEY: misc_feature

LOCATION: (1757)..()

OTHER INFORMATION: Xaa = any or unknown amino acid
US-10-150-821-4
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US-09-747-155-49
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US-09-911-842-4
                                                                                                             Sequence 49, Application US/09747155
Patent No. US20020151692A1
GENERAL INFORMATION:
APPLICANT: Rouquier, Sylvie
APPLICANT: Giorgi, Dominique
TITLE OF INVENTION: No. US20020151692A1el Polypeptides and Nucleic Acids Encoding
FILE REFERENCE: 19904-008 (C00986334US)
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SOFTWARE: PatentIn version 3.0 SEQ ID NO 49
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Best Local
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PRIOR FILING DATE: 2000-08-01
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATAMATA
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                              CURRENT APPLICATION NUMBER: US/09/747,155
CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/171,746
PRIOR FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Elliott, Gary S.
TITLE OF INVENTION: C3B/C4B COMPLEMENT RECEPTOR-LIKE MOLECULES AND USES THEREOF FILE REFERENCE: 01017/37592
CURRENT APPLICATION NUMBER: US/09/911,842
CURRENT FILING DATE: 2001-07-24
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TYPE: PRT
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10; Conservative
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62.5%;
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62.5%;
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Pred. No.
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APPLICANT: Recipor, Herve
APPLICANT: Chen, Sei-Yu
APPLICANT: Chen, Sei-Yu
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
ITITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot
FILE REFERENCE: DEX-0273
CURRENT APPLICATION NUMBER: US/10/001,857
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/252,054
PRIOR FILING DATE: 2000-11-20
INUMBER OF SEQ ID NOS: 208
SOFTWARE: Patentin version 3.1
SEQ ID NO 196
LENGTH: 310
TYPE: PRT
ORGANISM: Homo sapien
Search completed: June 25, 2003, 17:18:51 Job time: 2.32438 secs
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US-10-001-857-196
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Publication No. US20020183500A1
GENERAL INFORMATION:
APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
                                                                                                                                                                              Query Match 54.7%; Score 41; DB 9; Length 310; Best Local Similarity 66.7%; Pred. No. 94; Matches 10; Conservative 1; Mismatches 4; Indels
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125 SHSLLCVLPPSLSLS 139
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85 SILCSPLQSI 94
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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   seq length: 0 seq length: 2000000000
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ALIGNMENTS

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A:Status: preliminary
A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-490 <ALC>
A:Cross-references: EMBL:AL049711; GSPDB:GN00061; ATSP:F4F15.280
A:Experimental source: cultivar Columbia; BAC clone F4F15
                                                                                            A;Cross-references: GB:AE005174; NID:g12514746; PIDN:AAG55927.1; GSPDB:GN00145; UWGP:
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
                                                                                                                                                                                                                                                                                                                                 C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: C85683
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C85683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Alcaraz, J.P.; Clabault, G.; Cottet, A.; Mache, submitted to the Protein Sequence Database, April A;Reference number: 225015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein F4F15.280 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: T49096
                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-117 <STO>
A; Cross-references: GB:
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                                                                                                                                                                                                                                                                     R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                         probable IS encoded protein z1827 [imported] - Escherichia coli (strain 0157:H7, C; Species: Escherichia coli
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                                                                               A; Gene:
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                61.3%;
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Score 46; DB Pred. No. 2.2; 4; Mismatches
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Pred. No. 2.
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2.2;
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A; Title:
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A:Title: A human phosphatidylinositol 3-kinase complex related A:Reference number: S57219; MUID:95354652; PMID:7628435
A:Accession: S57219
                                                                    C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision
C:Accession: A72535
                                                                                                                                                                                                                                                                                                                                                   A:Map position: segment S
C:Superfamily: bunyavirus nonstructural protein
C:Keywords: nonstructural protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Description: converts ATP and 1-phosphatidyl-1D-myo-inositol to ADP and 1-phosphatidyl A;Pathway: required for vacuolar sorting and segregation; involved in both internalization A;Note: specific for phosphatidylinositol, inactive on phosphatidylinositol-3-phosphate C;Superfamily: slime mold phosphatidylinositol 3-kinase C;Keywords: phosphotransferase; protein trafficking
                R;Kawarabayasi, Y.; Hino, Y.; Jawa, H.; Takamiya, M.; Masuda, Bona Res. 6, 83-101, 1999
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                                                                                                        hypothetical protein APE1566 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
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A; Residues: 1-91 <AKA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Akashi, H.; Gay, M.; Ihara, T.; Bishop, D.H.L.
Virus Res. 1, 51-63, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999 C;Accession: S07943
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A; Residues: 1-887 < VOL>
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57.1%;
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                                  Horikawa, H.; Yamazaki, S.; Hai)
, S.; Funahashi, T.; Tanaka, T.;
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   aerobic
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rson, J.; Khalak, H.; Richardson, D.; Howell, they, L.; Weidman, J.; Smith, H.O.; Venter, J Science 281, 375-388, 1998
                                                C; Accession: H71345
R; Fraser, C.M.; Norris,
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A; Residues: 1-141 <SIM>
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8; Conser
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                                  S.J.; Weinstock, G.M.; White, O.; Sutton, ichardson, D.; Howell, J.K.; Chidambaram,
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54.5%;
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57.1%;
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R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; E. Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C. F.G.; Nunes, L.R.; Oliveira, M.A.; de Roliveira, R.C.; Ge Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, M.A.; Verjovski-Almeida, S.; Vettore, A.L., M.F.; Acagas, A.G., Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L., M.F.; Acagas, A.G., Vertore, A.L.
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A; Residues: 1-114 <KAW>
A; Cross-references: DDBJ:AP000062; NID:g5105244; PIDN:BAA80566.1; PID:d1044352; PID:g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: The genome sequence of the plant pathogen Xylella fastidiosa A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein XF0131 (imported) - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE003866; GB:AE003849; NID:g9104906;
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Score 42; DB Pred. No. 12; 3; Mismatches
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J.C.

M.; Utterback,

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A;Status, r. A;Status, r. A;Status, r. A;Status, r. A;Rolecule type: DNA A;Residues: 1-478 <COL>A;Residues: 1-478 <COL>A;Cross-references: GB:AE001208; GB:AE000520; NID:g3322538; A;Cross-references: Strain Nichols
A;Cross-references: EMBL;AC004680; NID:g3420043; PID:g3420049
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tall euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Ven Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: E84703
                                                                                                                                                                                                                                                                                              probable protein phosphatase 2C At2g30020 [imported] - Arabidopsis thaliana N;Alternate names: hypothetical protein F23F1.6 C;Specles: Arabidopsis thaliana (mouse-ear cress) C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 03-Jun-2002 C;Accession: T02483; E84703 R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, August 1998 s.;Description: Arabidopsis thaliana chromosome II BAC F23F1 genomic sequence. A;Reference number: 214675 A;Reference number: 214675 A;Reference number: 214675
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T41077
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A;Molecule type: DNA
A;Residues: 1-396 <ROU>
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A;Residues: 1-1010 <MCD>
A;Cross-references: EMBL.AL109957; PIDN:CAB53076.1; GSPDB:GN00068; SPDB:SPCC16A11.04
A;Experimental source: strain 972h-; cosmid c16A11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R:McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Zimmermann, W.; Wambutt, submitted to the EMBL Data Library, August 1999
A;Reference number: Z21822
A;Accession: T41077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: T41077 R; McDougall, R.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
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Similarity 62.5%;
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53.8%;
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Pred. No.
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Pred. No.
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R:Theologis, A:; ELNEL, Conn, L.; Conway, A.B., C.M.; Chung, M.K.; Conn, L.; Conway, A.B., C.M.; Chung, M.K.; Conn, L.; Conway, A.B., C.M.; Chung, M.K.; Conn, L.; Conway, A.B., C.; Khan, S.; Khaykin, A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, A.Authors: Hunter, J.L.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malti, R. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malti, R. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A.; Southwick, A.M.; Sun, A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A.; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
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T38130
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A:Map position: 2
A:Introns: 168/3
C:Superfamily: Arabidopsis thaliana hypothetical protein F7A7.220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Badcock, K.; Churcher, C.M.; Wood, V.; Barrell, B.G.; submitted to the EMBL Data Library, May 1997 A;Reference number: Z21772 A;Accession: T38130
                                                                A; Molecule type: DNA
A; Residues: 1-2123 <STO>
                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: F86348.
                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein F24J8.17 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-944 <BAD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: T38130
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C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-396 <S'
A; Map
                                         A;Cross-references: GB:AE005172; NID:g9454580; PIDN:AAF87903.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F86348
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Best Local
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Best Local Similarity
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les 9; Conserv
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Pred. No.
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1.1e+02;
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47;
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Maiti, R.; Marzia
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Query Match

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Score

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Length 2123

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RESULT 14
D96616
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D71557
                               hypothetical protein F19C14.10 [imported] - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: D96616
                                                                                                                                                                                                                                                                                       A; Experimental source: serotype D, C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                          A;Accession: D71557
                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein CT109 - Chlamydia trachomatis (serotype D, strain UW3/Cx) (Species: Chlamydia trachomatis C:Date: 13-Sep_1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999 C:Accession: D71557
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A;Residues: 1-262 <ARN>
A;Cross-references: GB:AE001284; GB:AE001273; NID:g3328494; PIDN:AAC67700.1;
A:Experimental source: serotype D, strain UW-3/Cx
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A;Residues: 1-247 <WIL>
A;Cross-references: EMBL:Z83231; PIDN:CAB05751.1; GSPDB:GN00020; CESP:F57G9.3
A;Experimental source: clone F57G9
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    R;Theologis,
Chin, C.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                          R; Stephens, R.S.; Kalman, Science 282, 754-759, 1998
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A;Map position: 2
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Best Local S
Matches 7
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 A.; Ecker, J
Chung, M.K.;
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                 J.R.;
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               Palm,
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Pred.
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C.J.; Federspiel,
Conway, A.B.; Conv
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 Conway, A.R.;
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               N.A.;
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                 Kaul,
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 Creasy, T.H.;
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                 S.; White, O.;
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               Alonso,
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Search completed: June 25, 2003, 17:17:36 Job time: 3.07383 secs

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A;Cross-references: EMBL:X17403; NID:g59591; PIDN:CAA35338.1; PID:e27303; PA;Note: this sequence was submitted to the EMBL Data Library, December 1989 A;Note: this reading frame extends between two stop codons and does not beg
                                                                                                                                                                                                                                                          A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-798 <CHE>
                                                                                                                                                                                                                                                                                                                       Curr. Top. Microbiol. Immunol. 154, 125-169, 1990 A;Title: Analysis of the protein-coding content of the sequence of A;Reference number: S09749; MUID:90269039; PMID:2161319 A;Accession: S09867
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C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
C;Accession: S09867
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S09867
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A;Molecule type: DNA
A;Residues: 1-313 <STO>
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Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin A; Authors: Li, J. Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, A; Mu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number; A86141; MUID:21016719; PMID:11130712
A; Accession: D96616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein UL102 - human cytomegalovirus C;Species: human cytomegalovirus, human herpesvirus
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                                                                                        Similarity
9; Conserv
                      SSSILCSPLPSLSLS 15
SSSVLSSALPSVTSS 745
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Pred. No.
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human herpesvirus 5
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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Maximum DB
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Gapop 10.0 ,
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PLAS_POPNI
PLAT_POPNI
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VG27_HSV11
YQ23_CAEEL
GLGB_SYNP7
RIR1.CRYPV
HUNB_MUSDO
KPB2_FUGRU
RI15_YEAST
MIG1_KLULA
EFTU_ARATH
FIG2_YEAST
GRO_RAT
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P43565
P570898
P170898
P170898
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Q44239
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P53907
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RESULT 2
OPRM_PIG
ID OPRW
AC 0952
DT 01-N
DT 01-N
DT 15-J
DE Mu-t
GN OPRW

OPRM_PIG STANDARD; PRT; 401 AA. 095247; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) Mu-type opioid receptor (MOR-1).

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Query Match Best Local S Matches 8

Local Similarity 57.1 es 8; Conservative

56.0%; 57.1%;

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gyh a collaboration EMBL outstation strictions on its strict in no way and for commercial b-sib.ch/announce/	erogro	Orthobunyavirus	homo sapien schistosoma homo sapien spinacia ol rattus norv agrobacteri arabidopsis drosophila ara musculu saccharomychomo sapien
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                                  HEPA_HCMVA
                                           RESULT
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Best Local
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HEPA_HCMVA
P16827;
01-AUG-1990
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                                                                                                                                        CARBOHYD
SEQUENCE
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DOMAIN
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DOMAIN
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PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
Phosphorylation; Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
entitles requires a license agreement (See http://www.isb-
or send an email to licenseelsb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa (Pig).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a coefficient the Swiss Institute of Bioinformatics and the EMBL
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8; Conserv
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401
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107
1147
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(Rel. 15, Created)
(Rel. 15, Last sequence
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                          STANDARD;
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106 C
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237
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                                                                                                                                        45098
                                                                                                                53.3%;
61.5%;
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CYTOPLASMIC (P
6 (POTENTIAL).
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N-LINKED
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Pred. No.
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5 (POTENTIAL)
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CYTOPLASMIC (POTENTIAL)
BY SIMILARITY.
PALMITATE (POTENTIAL).
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                          PRT;
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D (GLCNAC. .) (POTENTIAL).
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                          798 AA.
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                                                                                                           DB
18;
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P31170;

P31170;

01-JUL-1993 (Rel. 26, Created)

01-JUL-1993 (Rel. 26, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

5mall heat shock protein, chloroplast precursor.

HSP21 OR AT4G27670 OR T29A15.160.

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Traspermatophyta; Magnoliophyta; eudicotyledons; core eudicustis in Brassicales; Brassicaceae; Arabidopsis.
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                                                            Mol.
                                                                                                                                                                                Chen
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                                                                                                                                                                                              STRAIN=cv. Columbia; TISSUE=Leaf; MEDLINE=91246118; PubMed=2038305;
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DNA replication
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                                                                        MEDLINE=91360086; PubMed=1886617; Chen Q., Vierling E.;
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X17403; CAA35338.1; -.
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                                                                                                                                                                  "Analysis of conserved domains identifies
                                                                                                                                                                                                                                                       NCBI_TaxID=3702;
                                                                                                                                   chloroplast heat shock protein.";
Gen. Genet. 226:425-431(1991).
                                                                                                                                                                                Q., Vierling E.;
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                                                          228:328-328(1991).
 PubMed=8391109
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RA Langham S. A., McCullagh B., Bilham L., Robben J., Vandenbussche F.,
RA Van der Schweren J., Grymonprez B., Chuang Y. J., Vandenbussche F.,
RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defor E.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Holzer E., Brandt A., Peters S., Van den Daele H.,
RA De Keyser A., Buysshaert C., Gielenn J., Villarroel R., De Clercq R.,
RA Petert A., Rajandream M., Lyne M., Benes V., Rechmann S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
RA Petert A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Dose S., de Haan M., Marse A.C., Schaefer M., Mueller-Auer S.,
RA Dose S., de Haan M., Marse A.C., Schaefer M., Mueller-Auer S.,
RA Massenet O., Ouidgley F., Clabauld G., Nuendelein A., Ferber R.,
RA Massenet O., Ouidgley F., Clabauld G., Nuendelein A., Felber R.,
RA Massenet O., Ouidgley F., Clabauld G., Nuendelein A., Felber R.,
RA Glabons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Glabons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francs P., Bielke C.,
RA Heijnen L., Schwarz S., Scholler P., Cordes M., Abu-Threideh J.,
RA Schon M., Murray J., Sheet P., Cordes M., Abu-Threideh J., Stocker S.,
RA Klamer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Kamer J., Fulton L., Mardis E., Dante M., Pepin K., Johnson D.,
RA Kamer J., Fulton L., Mardis E., Dante M., Pepin K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Altonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Mar L., Scholz N., Rodriguez M., Hoffman J., Till S.,
Ra Clant S., Shah R.,
Sehon M., Martlenssen R., McComble W. R.,
Thalland R., Shah R.,
Sehon M., Martlensen R., McComble W. R.,
Thalland R., Scholand R., Shah R.,
Seho
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   severe
                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 402:769-777(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kreis M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20083488;
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                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Exeuropean Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                               SIMILARITY: PLANTS HAVE FOUR CLASSES OF HSP20: CLASS I AND II WHICH ARE CYTOPLASMIC; CLASS III WHICH IS IN THE CHLOROPLAST AND CLASS IV WHICH IS IN THE ENDOMEMBRANE. THIS PROTEIN BELON
                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                            CLASS III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heat stress,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           t B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
S.-A., McCullagh B., Bilham L., Robben J.,
Schupren J. Grumonannan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ng K.W., Sundberg H., Vierling E.;
tail length of a heat shock protein RNA is increased by
eat stress, but intron splicing is unaffected.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239:323-333(1993).
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                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                             Chloroplast.
O THE SMALL HEAT SHOCK PROTEIN (HSP20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wambutt R.,
                                                                                                                                                                                                                                                                               ENDOMEMBRANE. THIS PROTEIN BELONGS
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d and this statement is not removed. Usage by and for commercial s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                               non-profit institutions as long as its content
                                                                                           restrictions
                                                                                                       a collaboration
MBL outstation -
                                                                                                      outstation
                                                                               50
modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                     TRANSFAC; T01066; -. FlyBase; FBgn0003300;
                                                     EMBL; X56432; CAA39817.1;
PIR; A36392; A36392.
PF00853;
                                           060472;
           IPR000040;
                                            1CMO.
        AML1_Runt.
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SIMILARITY: CONTAINS 1 RUNT DOMAIN

EMBRYOGENESIS

STAGE: MOST

ABUNDANTLY EXPRESSED AT

THE BLASTODERM

EMBL; X54102; CAA38036.1; -. EMBL; M94455; AAA32818.1; -. EMBL; AL161571; CAB81417.1;

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RESULT 5
RUNT_DROME
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Best Local
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PIR; S16527; S16527.
PIR; S16005; S16005.
PIR; S35240; S35240.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RUNT_DROME
P22814;
01-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                              Kania M.A., Bonner A.S., Duffy J.B., Gergen J.P.; "The Drosophila segmentation gene runt encodes a novel nuclear regulatory protein that is also expressed in the developing ne
                                                                                                                                                                                                                                               system."
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1991
15-JUN-2002
                                                 -1- FUNCTION: PLAYS A PÍVOTAL ROLE IN REGULATING THE EXPRESSION OF OTHER PAIR-RULE GENES SUCH AS EVE, FTZ, AND H.
-1- SUBCELLULAR LOCATION: NUCLEAR.
-1- TISSUE SPECIFICITY: DEVELOPING CENTRAL AND PERIPHERAL NERVOUS
                                                                                                                       Nature 356:484-484(1992)
                                                                                                                                                          MEDLINE-92220161; Pu
Daga A., Tighe J.E.,
                                                                                                                                                                                            SIMILARITY TO AML1
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=91065517; PubMed=2249771;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly)
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PROSITE; PS01031; HSP20; 1
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                                                                                                                                          Leukaemia/Drosophila
DEVELOPMENTAL
STAGE OF EMBRY
                                    SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 shock; Chloroplast; Transit peptide. 1 19 CHLOROPLAST
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AASALCSPLAPSPSVS.
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19, Last
41, Last
                                                                                                                                                          PubMed=1560822;
E., Calabi F.;
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62.5%;
                                                                                                                                        homology.";
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SMALL HEAT SHOCK PROTEIN.
; B25400AF6C01972E CRC64;
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Pred. No. 12;
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Best Local S
Matches
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ATP-binding;
DOMAIN
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VARIANT
                                                                                                                                                                                                                  use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nanba E., Suzuki K.;
"Organization of the mouse acid beta-galactosidase gene.";
"Biochem. Biophys. Res. Commun. 178:158-164(1991).
-!- FUNCTION: CLEAVES BETA-LINKED TERMINAL GALACTOSYL RESIDUES FROM
GANGLIOSIDES, GLYCOPROTEINS, AND GLYCOSAMINOGLYCANS.
-!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing beta-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Beta galactosidase precursor (EC 3.2.1.23) (Lactase) (Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular cloning of mouse acid beta-galactosidase cDNA: sequence, expression of catalytic activity and comparison with the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLB1 OR GLB-1 OR BGL.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nanba E., Suzuki K.;
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SIMILARITY: BELONGS TO FAMILY 35 OF GLYCOSYL HYDROLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                         galactose residues in beta-D-galactosides
                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the En
                                                                 M57734;
M75122;
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|22 SPSILCSALPN 132
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                                           AAA37292.1;
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AAA37292.1;
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72.7%;
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Sciurognathi; Muridae;
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35;
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                                                                                                                                                                                                                                                                                                      restrictions
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                                                                                                                                                                                                                                                                                                                             EMBL
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                                                                                                                                                                                                                                                                                                                                 collaboration -
L outstation -
                                                                                                                                                                                                                                                                                                                               outstation
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AABI_MOUSE STANDARD,

QSWV76;

16-OCT-2001 (Rel. 40, Created)

T 16-OCT-2001 (Rel. 40, Last sequence update)

T 16-OCT-2001 (Rel. 40, Last annotation update)

Mapter-related protein complex 4 beta 1 subunit

A AP-4 adapter complex beta subunit).
                                                                                                                                                                                                                                                                                                     A4B1_MOUSE
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Matches 7
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CONFLICT
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ACT_SITE
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MEDLINE=99355166; PubMed=10436028;

Hirst J. Bright N.A., Rous B., Robinson M.S.;

"Characterization of a fourth adaptor-related Mol. Biol. Cell 10:2787-2802(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001944; GH_35.

Pfam; PF01301; GLyco_hydro_35; 1.

PRINTS; PR00742; GLYCOSYL_HYDROL_F35;

PROSITE; PS01182; GLYCOSYL_HYDROL_F35;
                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                            Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROPEP
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                              SIMILARITY).

SIMILARITY).

SUBUNIT: ADAPTER-LIKE COMPLEX 4 (AP-4) IS AN HETEROTETRAMER COMPOSED OF TWO LARGE CHAINS (EPSILON/AP4E1 AND BETA/AP4B1), MEDIUM CHAIN (MU/AP4M1) AND A SMALL CHAIN (SIGMA/AP4S1).

MEDIUM CHAIN (MU/AP4M1) ASSOCIATED WITH THE TRANS-GOLGI NETWOR
                                                                                . Biol. Cell 10:2787-2802(1999).
FUNCTION: SUBUNIT OF NOVEL TYPE OF CLATHRIN-OR NON-CLATHRIN-ASSOCIATED PROTEIN COAT INVOLVED IN TARGETING PROTEINS FROM PROMISE OF CHAIL SUBURY OF THE ENDOSOMAL-LYSOSOMAL SYSTEM
                 SUBCELLULAR LOCATION: SIMILARITY).
SIMILARITY: BELONGS TO
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5 LCTPLPLLAL
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7; Conservative
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                                                                                                                                                                                                           (Mouse)
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                                                                                                                                                                                      Chordata;
Rodentia;
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70.0%;
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                  THE ADAPTOR
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N-LINKED (GLCNAC. .
N-LINKED (GLCNAC. .
N-LINKED (GLCNAC. .
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOPHILE (POTENTIAL)
N-LINKED (GLCNAC. . .)
                                                                                                                                                                                       Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BETA-GALACTOSIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                         -> D (IN REF. 2)
-> R (IN REF. 2)
0E68EAA66A10803A
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Signal; Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                          DB 46;
                  COMPLEXES
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                                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
                  LARGE SUBUNITS
                                                                                                                                                                                                                                        (Beta
                                                                                                                                                                                                                                                                                                                                                                                  Indels
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;; Murinae; Mus
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RESULT 8
YNO4_YEAST
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Best Local
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                                                                                                                                                                                                                                                                               STRAIN-S288c / FY1679;
STRAIN-S288c / FY1679;
MEDLINE-96287653; PubMed-8686380;
Nasr F., Becam A.-M., Herbert C.J.;
"The sequence of 36.8 kb from the left arm of chromosome XIV reveals
"The sequence of 36.8 kb from the left arm of chromosome XIV reveals
24 complete open reading frames: 18 correspond to new genes, one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mallet L., Bussereau F., Jacquet M.;
"A 43.5 kb segment of yeast chromosome XIV, which contains MFA2,
MEP2, CAP/SRV2, NAM9, FKB1/FPR1/RBP1, MOM22 and CPT1, predicts addenosine deaminase gene and 14 new open reading frames.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Hypothetical 84.2 kDa protein in MFA2-MEP2 intergenic region.
YNL144C OR N1205 OR N1790.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                             EMBL; Z46843; CAA86882.1;
EMBL; X92517; CAA63294.1;
EMBL; Z71420; CAA96027.1;
SGD; S0005088; YNL144C.
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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P53907;
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Hypothetical SEQUENCE 7
                                                                                                                                                                                                                                                                   Yeast 12:169-175(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                 adenosine deaminase gene and
Yeast 11:1195-1209(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4932;
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InterPro; IPR002553; Adaptin_N.
                                                                                                                                                                                                                                               SIMILARITY: TO YEAST YHR131C
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739 AA;
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al protein
740 AA; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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39 AA; 82618 MW;
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84202 MW;
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Pred. No. 53;
7A3D75999DC83D06 CRC64;
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   Matches
                        Query Match
Best Local
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Banfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortlmore B., O'Callaghan M.
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Sins M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
Wahldman P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1993 (Rel. 25, Created)
.01-FEB-1995 (Rel. 31, Last sequence update)
.15-JUN-2002 (Rel. 41, Last annotation update)
Probable 3',5'-cyclic phosphodiesterase R08D7.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this scatement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
Rhabditidae; Peloderina
                                                                                                                                                                                                                                                                                    WormPep; R0BD7.6; CE01047.
InterPro; IPR003018; GAF.
InterPro; IPR003607; ME_Pplase_HDc.
InterPro; IPR002073; PDEase.
Pfam; PF00233; PDEase; 1.
Pfam; PF01590; GAF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Bristol N2;
MEDLINE=94150718; PubMed-7906398;
                                                                                                           PROSITE; PS00126; PDEASE_I; 1.
Hypothetical protein; Hydrolase;
SEQUENCE 918 AA; 104238 MW;
                                                                                                                                                                                                 PRINTS; PR00387; PDIESTERASE1.
SMART; SM00065; GAF; 1.
SMART; SM00471; HDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S24462; S24462.
PIR; S41041; S41041.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 368:32-38(1994).
-!- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; 212017; CAA78052.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "2.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleoside 5'-phosphate.
SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
FAMILY. STRONG, TO MAMMALIAN TYPE 6 CGMP PHOSPHODIESTERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42
                        Similarity
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                     52.0%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.0%;
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                        Score 39; DB Pred. No. 67;
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Pred. No. 53;
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MU3C_ANASP STANDARD; PRT; 120 AA

Q44239; Q9WVX6;

01-NOV-1997 (Rel. 35, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Howitt C.A., Whelan J., Price G.D., Day D.A.; "Cloning, analysis and inactivation of the ndhk gene encoding a subunit of NADH quinone oxidoreductase from Anabaena PCC 7120."; Eur. J. Biochem. 240:173-180(1996).

-i- CATALYTIC ACTIVITY: NADH + plastoquinone - NAD(+) + plastoquinol.
-i- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 3 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.; "Complete genomic sequence of the filamentous nitrogen-fixing Cyanobacterium Anabaena sp. strain PCC 7120."; DNA Res. 8:205-213(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SPECIES-A.sp. PCC 7120;
MEDLINE-21595285; PubMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Isolation and characterisation of the ndhCKJ-cluster of cyanobacteria Anabaena sp. PCC 7120."; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SPECIES-A.variabilis; STRAIN-PCC 7937 / ATCC 29413;
Happe T., Schiefer W., Boehme H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NADH-plastoquinone NDHC OR ALL3842.
   SEQUENCE
                         InterPro; IPR000440; Oxidored_q4.
Pfam; PF00507; oxidored_q4; 1.
Oxidoreductase; NAD; Plastoquinone; Complete
CONFLICT 87 87 H -> N (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES=A.sp. PCC 7120;
MEDLINE=96390878; PubMed=8797851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaneko T., Wakamura Y., Wolk C.P., Kuritz T., Sasamoto
Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Ki
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES-A.sp. PCC 7120;
Happe T., Schiefer W., Boehme H.;
                                                                                                                                                           EMBL; U31208;
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NCBI_TaxID=103690, 1172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anabaena variabilis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 84-120 FROM N.A. SPECIES-A.sp. PCC 7120;
                                                                                                                                                                              AJ012180; CAB45639.1; -. AP003594; BAB75541.1; -. AJ012181; CAB45646.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (OCT-1998) to
   120 AA;
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   13621 MW;
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   574B662EAFF69BB2 CRC64;
                                   proteome.
3).
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a K., Kimura
, Muraki A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of Anabaena
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GRHR_SHEEP
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                                                                                                                                        RESULT 12
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APC4_MOUSE
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Best Local
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                                                     P32237;
O1-OCT-1993 (Rel. 27, C:
O1-OCT-1993 (Rel. 27, L:
15-DEC-1998 (Rel. 37, L:
Gonadotropin-releasing )
                                                                                                                                                                                                                                                                    CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                     EMBL;
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                              GNRHR.
                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STORE TISSUE=Liver;
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                                                                                                                                                                                                                                                                                                     SIGNAL
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Apolipoprotein C-IV precursor (Apo-CIV) (Apolipoprotein C2-linked)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APC4_MOUSE
                                                                                                                                                                                                                                                                                           CHAIN
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Caprinae;
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107
124 AA;
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27, Last sequence update)
37, Last annotation update)
asing hormone receptor (GNRH-R)
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107
14288
 Ovis.
           Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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97C3CDEE72C9A452 CRC64;
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EMBL; L22215; AAC37336.1; -.
EMBL; X72088; CAA50978.1; -.
EMBL; X42937; AAB38515.1; -.
EMBL; L43842; AAB41939.1; -.
EMBL; L43842; AAB41939.1; JOINED.
EMBL; L43841; AAB41939.1; JOINED.
PIR; JN0882; JN0882
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94059099; PubMed=7694577;
Illing N., Jacobs G.F.M., Becker I.I., Flanagan C.A., Davidson Eales A., Zhou W., Sealfon S.C., Millar R.P.;
"Comparative sequence analysis and functional characterization cloned sheep gonadotropin-releasing hormone receptor reveal differences in primary structure and ligand specificity among mammallan receptors.";
          CARBOHYD
CARBOHYD
                                                          DOMAIN
TRANSMEM
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-Scottish blackface; TISSUE-Pituitary;
MEDLINE-94040345; PubMed-8224516;
Brooks J., Taylor P.L., Sauders P.T.K., Eidn
                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                This
                                                                                                                                                                                                                                                                                                                                                                                                                                 Campion C.E., Turzillo A.M., Clay C.M.;
"The gene encoding the ovine gonadotropin-releasing hormone receptor: cloning and initial characterization.";
Gene 170:277-280(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hormone receptor and clestrous cycle.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem.
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   DISULFID
                                       TRANSMEM
                                                                               TRANSMEM
                                                                                                                                                                                          PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McNeilly A.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-9940;
                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Integral membrane SIMILARITY: BELONGS TO FAMILY 1 OF G-PRC
                                                                                                                                                                                                                                                                                                                                           European
                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: THIS RECEPTOR MEDIATES ITS ACTION BY ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
                                                                                                                                                                                                                                                                                                                                                                                                      MESSENGER SYSTEM.
                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                    00001; 7tm_1; PS00237; G_P
                                                                                                                                                                                            PS50262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biophys. Res. Commun. 196:745-751(1993).
                                                                                                                                                                                coupled
Bioinformatics Institute.
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receptor;
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102
                                                                                                                                                                               G_PROTEIN_RECEP_F1_1; 1.
G_PROTEIN_RECEP_F1_2; 1.
receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94:R23-R27(1993)
                                                        5 (POTENTIAL).
CYTOPLASMIC (PO
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
BY SIMILARITY.
                                        EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
                                                                              EXTRACELLULAR (POTENTIAL) 5 (POTENTIAL).
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                                                                                                            CYTOPLASMIC
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                                                                                                                              EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                    ransmembrane; Glycoprotein.
EXTRACELLULAR (POTENTIAL).
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                                                                   (POTENTIAL).
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Best Local Similarity
Matches 10; Conser
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Pfam: PF00572: HAMP: 1.
Pfam: PF00578: HAMPase_c: 1.
Pfam: PF002518: HATPase_c: 1.
PRINTS: PR00344: BCTRLSENSOR.
SMART: SM00304: HAMP: 1.
SMART: SM00388: HATPase_c: 1.
SMART: SM00388: HiskA: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Identification and characterization of a two-component regulatory system involved in invasion of eukaryotic cells and heavy-metal resistance in Burkholderia pseudomallei.";

Infect. Immun. 65:4972-4977(1997).

-i- FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM IRLR/IRL MAY BE INVOLVED IN INVASION OF EUKARYOTIC CELLS AND HEAVY-METAL RESISTANCE. PROBABLY ACTIVATES IRLR BY PHOSPHORYLATION.

-i- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
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15-DEC-1998 (Rel. 37, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Sensor protein irlS (EC 2.7.3.-).
                                                                                                 PROSITE; PS50109; HIS_KIN; 1. Sensory transduction; Transferase; Kinase;
                                                                                                                                                                                                                                                   EMBL; AF005358; AAB92483.1; -.
InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR004358; Bact_sens_pr_C.
InterPro; IPR003660; HAMP.
InterPro; IPR004359; HIS_KIN_sig.
InterPro; IPR003661; His_kinA.
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                                                                                   Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
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                                 DOMAIN
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SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaborative the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                   Inner membrane;
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beta subdivision; Burkholderia
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              POTENTIAL.
CYTOPLASMIC
POTENTIAL.
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Pred. No.
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0618374F33ECC6FE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                   Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
AS Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
AR Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
AR Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
AR Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
AR Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
AR Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Hodgson G.,
AR Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
AR James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
AR Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
AR Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
AR Multer K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
AR Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
ARA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
Araylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
ARA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
ARA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
ARA Woodward J., Volckaert G., Holzer E., Moestl D., Hilbert H.,
ARA Woodward J., Volckaert G., Holzer E., Moestl D., Hilbert H.,
ARA Woodward J., Volckaert G., Holzer E., Weestl D., Hilbert H.,
ARA Woodward J., Vanneyer J., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
ARA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
ARA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
ARA Lucas M., Rochet M., Galllardin C., Tallada V.A., Garzon A., Thode G.,
ADDA BARA, Cruzado L., Jimenez J., Sanchez M., Gersburg S.L.,
ARA Cerrutti L., Lowe T., McComble W.R., Paulsen I., Potashkin J.,
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SEQUENCE
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
            This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                     Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Pot Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; "The genome sequence of Schizosaccharomyces pombe."; Nature 415:871-880(2002).
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                                                                                                                                                                                                                     MEDLINE-98162722; PubMed-9501991; Yoshioka S., Kato K., Nakai K., O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
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                                                                                                             Res. 4:363-369(1997).
SUBCELLULAR LOCATION: Integral membrane protein (Potential).
SIMILARITY: BELONGS TO THE AMINO ACID PERMEASE FAMILY.
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Pred. No.
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C4FE275489AEDCBD CRC64;
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  and
                                                        a collaboration - MBL outstation
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                       "Sequence
thaliana."
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Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
Spermsids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                            TRPX_ARATH STANDARD; PRT; 621 AA p32069; 01-OCT-1993 (Rel. 27, Created) 01-OCT-1993 (Rel. 27, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 16-JUN-2002 (Rel. 41, Last annotation update)
   Nature
                                                       Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.F., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Fu Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo I Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S. Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Crea Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fras
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(EC 4.1.3.27)
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                                                                                                                                       MEDLINE=20083487; PubMed=10617197;
                                                                                                                                                                                       "Two anthranilate synthase genes in Arabidopsis: defense-related regulation of the tryptophan pathway."; plant Cell 4:721-733(1992).
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                                               Venter J.C.
                                                                                                                                                                 SEQUENCE FROM N.A.
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Pro; IPR002293; AAC_rel_prmease1.
Pro; IPR004840; AAC_permease.
Pro; IPR004841; Permease.
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7; Conservat
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                                   and analysis of chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L protein; 68 88 126 126 126 129 206 22 288 30 397 41 1492 5] 293 29 395 31 31 3 31 3 37 2 3 372 3 372 3
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A -> D (IN REF. 2).

VMFL -> RHVFI (IN REF. 2).

MISSING (IN REF. 2).

A -> G (IN REF. 2).

P -> A (IN REF. 2).

A -> D (IN REF. 2).
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                                   plant Arabidopsis
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                                                                                Creasy T.H.,
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                                                                                           S., Umayam L.,
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                                                                                                                            Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                          InterPro; IPR005256; Anth_synthI.
InterPro; IPR000350; Chorismate_bind.
Pfam; PF00425; Chorismate_bind; 1.
PRINTS; PR000955; ANTSNTHASEI.
ProDom; PD000779; Chorismate_bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                          Tryptophan biosynthesis; Lyase; Chloroplast; Transit peptide; multigene family.
                                                                                                                                                                                                                                                                     ProDom; PD000779; Chorismate_bind; 1.
TIGREAMS; TIGR00564; trpE_most; 1.
                                                                                                                                                                                                                                                                                                                                                                          EMBL; M92354; AAA32739.1; -.
EMBL; AC005496; AAG35228.1; -.
PIR; S27752; S27752.
HSSP; Q06128; 1QDL.
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PATHWAY: Tryptophan biosynthesis; first step.

SUBUNIT: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II.

SUBCELLALAR LOCATION: Chloroplast (Probable).

SUBCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FAMILY.
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                                                                                 SILCSPLPSLSLS 15
                                                              SIKCSYTPSLDLS
                                                                                                                                                                                              621 AA;
                                                                                                                               Conservative
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69815 MW;
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69.2%;
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                                                                                                                                              Score 38; DB 1; Pred. No. 65;
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ANTHRANILATE SYNTHASE COMPONENT I-2
                                                                                                                                                                                            D4039FE58A420967 CRC64;
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                                                                                                                                                            Length 621;
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Perfect score:
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                    Score
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  length: 0
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                          Q15134 homo sapien
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Q96eh4 homo sapien
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Q9jms9 escherichia
Q8x3q9 escherichia
Q9maa0 arabidopsis
Q8w0z7 arabidopsis
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peaton			ω	40	
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Q8qz43 sango virus			ω	40	
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Q8tfe4 gaeumannomy			. 7	41	
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Q9ad17 polyangium			. 7	41	
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Q9ph15 xylella	16 Q9PH15			42	

ALIGNMENTS

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RESULT 2
Q8R4H6
ID Q8R4
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Q9SUY8;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 53.0 kDa protein.
F4F15.280.
    Q8R4H6
                                                                                                                                                                                                                                                                  Hypothetical protein. SEQUENCE 490 AA;
                                                                                                                                                                                                                                                                                                         EU Arabidopsis sequencing project; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases EMBL; AL049711; CAB41337.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Alcaraz J.P., Clabault G., Cottet A., Mache R., Mewes H.W., Mayer K.F.X., Quetier F., Salanoubat M.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
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11; Conservative
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    PRELIMINARY;
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73.3%;
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Pred. No.
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*Activation of Clg, a Novel Dbl Family G Factor Gene, by Proviral Insertion at Evin B Cell and Myeloid Leukenias.";
J. Biol. Chem. 277:13463-13472(2002).
EMBL; AF465238; AAL93134.1;
EMBL; AF465238; AAL93134.1;
SEQUENCE 1298 AA; 139193 MW; 3451F4F
SEQUENCE FROM N.A.

MEDIJINE-95337425; PubMed-7612932;

Broom J.E., Hill D.F., Hughes G., Jones W.A.,

Stockwell P.A., Petersen G.B.;

"Sequence of a transposon identified as Tn1000
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01-JUN-2002
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Saadi S., Maas W.K., Hill D.F., Bergquist P.L.;
"Nucleotide sequence analysis of RepFIC, a basic
IncFI plasmids P307 and F, and its relation to th
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"F Plasmid
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MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burlar
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EMBL; AP001918; BAA97892.1; -
Plasmid; Complete proteome.
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MEDLINE=94359430; PubMed=7915817;
Topen-Ihler K., Skurray
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J. Bacteriol. 165:1043-1045(1986).
                                                          EMBL; AE005326; AAG55927.1; -.
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Best Local
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                                           SEQUENCE FROM N.A.

Cheuk R., Chen H., Kim C.J., Meyers M.C., Banh J., Bowser L.,
Cheuk R., Chen H., Kim C.J., Meyers M.C., Banh J., Bowser L.,
Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jones T., Kamiya A., Karlin Neumann G., Kawai J., Lam B.,
Ishida J., Jones T., Kamiya A., Karlin Neumann G., Kawai J., Lam B.,
Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
Palm C.J., Ouach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.
Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
"Arabidopsis CDNA clones.";
"Arabidopsis CDNA clones.";
                                                                                                                                                                                                                                                                                                                                                      Q8W0Z7;
                                                                                                                                                                                                        (AT3905190/T12H1_16).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidenuosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative branched-chain amino acid aminotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D. Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M., "Arabidopsis thaliana chromosome III BAC T12H1 genomic sequence.", "Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AC00317; AAF27025.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eveurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01063; aminotran_4; 1.
ProDom; PD001961; Aminotran_4; 1.
Aminotransferase; Transferase.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative branched-chain amino acid aminotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001544; Aminotran_4.
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                                                                                                                                                                                                  NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
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                                 (DEC-2001)
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                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                            the EMBL/GenBank/DDBJ databases
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Pred. No. 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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7.7;
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Best Local
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Best Local
                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001882; Biotin_attach.
InterPro; IPR000089; Biotin_lipoyl.
InterPro; IPR000089; Biotin_lipoyl.
InterPro; IPR0000901; CPSase
Pfam; PF02785; Biotin_carb_C; 1.
Pfam; PF00289; CPSase_L_chain; 1.
Pfam; PF00289; CPSase_L_D2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q91ZA3; PRELIMINARY; PRT; /24 AA.
Q91ZA3;
O1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LUMBLE CONTROL OF THE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Propionyl Coa....
Mus musculus (Mouse).
Mus musculus (Motazoa; Chordata;
""" Netazoa; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bowser L., Carninet P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann Kawai J., Lam B., Led J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Sat Seki M., Southwick A., Tang C.C., Torlumi M., Wu H.C., Yamada K Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis
                                                                                                                                                                                                                                                                                   PROSITE; PS00188; BIOTIN; UNKNOWN_1.
PROSITE; PS00866; CPSASE_1; UNKNOWN_1.
PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
SEQUENCE 724 AA; 79660 MW; DB5EC4CBF40739FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01063; aminotran_4; 1. ProDom; PD001961; Aminotran_4; 1. Aminotransferase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Biol. Chem. 0:0-0(2001).
EMBL; AY046947; AAL02364.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and its rescue by postnatal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Propionyl CoA-carboxylase alpha-subunit.
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InterPro; IPR001544; Aminotran_4.
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11; Conserv
                                                                                                                                             Similarity
8; Conserv
TSSTLCSPMPGVVVAV
                                                                        SSSILCSPLPSLSLSV 16
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50.0%;
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669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mice lacking propionyl-CoA carboxylase liver-specific supplementation via a
                                                                                                                                                                               Score 46; DB Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 46; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata;
Sciurognathi; Muridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     670A17B8D74B5D86 CRC64;
                                                                                                                                             Mismatches
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8.7;
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                                                                                                                                                                                                                  11;
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                                                                                                                                                                                                                  Length 724;
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                                                                                                                                             Indels
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RESULT Q922N3 ID Q9 AC Q9

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PRELIMINARY;

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Best Local
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Submitted (APR-2001) to the EMBL/GenB Submitted (APR-2001): 1; -.

InterPro; IPR001882; Biotin_attach. InterPro; IPR000089; Biotin_lipoyl. InterPro; IPR000091; CPSase. Pfam; PF02785; Biotin_carb_C; 1.
Pfam; PF002785; Biotin_lipoyl; 1.
Pfam; PF00289; CPSase_L_chain; 1.
Pfam; PF00289; CPSase_L_chain; 1.
Pfam; PF00613; PI3Ka; 1.

Pfam; PF00792; PI3K_C2; 1.

Pfam; PF00454; PI3_PI4_kinase; 1.

SMART; SM00239; C2; 1.

SMART; SM00145; PI3Ka; 1.

SMART; SM00146; PI3Kc; 1.

SMART; SM00142; PI3K_C2; 1.

SMART; SM00142; PI3K_C2; 1.

PROSITE; PS00915; PI3_4_KINASE_1; 1

PROSITE; PS00916; PI3_4_KINASE_3; 1

PROSITE; PS00916; PI3_4_KINASE_3; 1
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Q15134;
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01-DEC-2001 (TrEMBLrel. 19, La
01-JUN-2002 (TrEMBLrel. 21, La
Similar to propionyl coenzyme,
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-280 FROM N.A.

MEDLINE-95354652; PubMed-7628435;

Volinia S., Dhand R., Vanhaesebroeck B.,

Zvelebil M.J., Domin J., Panaretou C., Wa

A human phosphatidylinositol 3-kinase cc

Vps34p-Vps15p protein sorting system.";

EMBO J. 14:3339-3348(1995).
                                                                                                                                                                                                                                                                                                                                               Volinia S.;
Submitted (DEC-1994) to the
EMBL; Z46973; CAA87094.1; -
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01-NOV-1996 (TREMBLEGE: 01, La
01-DEC-2001 (TREMBLEGE: 19, La
Phosphatidylinositol 3-kinase.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                          InterPro; IPR000008; C2.
InterPro; IPR001263; PI3Ka.
InterPro; IPR002420; PI3K_C2.
InterPro; IPR000403; PI3_PI4_kinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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nes 8; Conserv
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PS00866; CPSASE_1; UNKNOWN_1.
PS00867; CPSASE_2; UNKNOWN_1.
724 AA; 79940 MW; 8B646617F9E399A2 CRC64;
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eutheria;
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    Created)
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    Carboxylase, alpha

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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complex related to
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RESULT 11
Q9N7D6
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Best Local :
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Q9N7D6;
Q1-OCT-2000
01-OCT-2000
01-MAR-2002
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Q8W6E1;
Q1-MAR-2002
Q1-MAR-2002
Q1-MAR-2002
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SEQUENCE
                                                                              Kinase.
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NON_TER
                                                                                                       Murphy L., Quail M., Harris D., R. Submitted (JUL-2000) to the EMBL/EMBL, AL39035; CACO1001.1; EMBL, RIPRO00719; Euk_pkinase. ProDom; PD000001; Euk_pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                               Sinha K.K., Ghosh A.; "Complete nucleotide sequence of single-stranded filamentous vibriophage VSKK."; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases... EMBL; AF452449; AAL40839.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                        Coat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Putative major coat protein. bacteriophage VSKK.
Viruses; ssDNA viruses; Inov VIRUSES CONTROL TAXID=180503;
                                                                    SEQUENCE
                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-FRIEDLIN;
                                                                                                                                                                                                  Leishmania major.
Eukaryota; Euglenozoa;
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01-CCT-2000 (TrEMBLrel. 15, Last
01-MAR-2002 (TrEMBLrel. 20, Last
101-MAR-2002 (TrEMBLrel. 20, Last
Possible serine/threonine kinase
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                                                                                                                                                                                        NCBI_TaxID=5664;
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                             Local Similarity hes 10; Conserv
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ENCE 82
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9; Conserv
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SSSILCSPLPSLSLS
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138 AA;
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                                       Score 43;
Pred. No.
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Pred. No.
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Pred. No.
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                                                                   2AF74AF4488B12D6 CRC64;
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annotation update)
pkn8 (Fragment).
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                                                                                                                                                                                                 Trypanosomatidae;
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4.7;
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                                               Length 138;
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Matches
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                                                        InterPro: IPRO00152; Asx_hydroxyl.
InterPro: IPR000561; EGF-like.
InterPro: IPR000742; EGF_2.
InterPro: IPR0001881; EGF_Ga.
InterPro: IPR001438; EGF_II.
InterPro: IPR001438; EGF_II.
InterPro: IPR001759; Pentaxin.
InterPro: IPR000436; Sushi_SCR_CCP.
InterPro: IPR0000436; Sushi_SCR_CCP.
InterPro: IPR0000436; Sushi_SCR_CCP.
        Pfam; PF00008; EGF; 10.
Pfam; PF002494; HYR; 2.
Pfam; PF00354; Pentaxin; 1.
Pfam; PF00084; Sushi; 33.
Pfam; PF00092; vwa; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
EMBL; BC01
SEQUENCE
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                Biochem. J. 352:49-59(2000).
EMBL: AF206329; AAG32160.1;
HSSP; P00740; IEDM.
MGD; MGI:1928849; Polydom.
                                                                                                                                                                                                                          MEDLINE=20517255; PubMed=11062057; Gilges D., Vinit M.-A., Callebaut I.,
                                                                                                                                                                                                                                       STRAIN-C3H/HENSIC; MEDLINE-20517255;
                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                              Q9ES77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
Similar to RIKEN cDNA 4933430F08 gene.
                                                                                                                                                                                                 protein,
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                              Polydom protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-LUNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q96EH4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q96EH4
                                                                                                                                                                                                                    Romeo P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-9606;
                                                                                                                                                                                                           "Polydom :
                                                                                                                                                                                                                                                                              NCBI_TaxID-10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tted (AUG-2001) to the EMBL/GenBank/DDBJ databases
BC012330; AAH12330.1; -.
NCE 189 AA; 19503 MW; BC1D0F5B688D62E7 CRC64;
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  EGFBLOOD
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71.4%;
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Pred. No.
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nd von willebrand
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SMART; SM00032; CCP; 34.
SMART; SM00181; EGF; 15.
SMART; SM00179; EGF_CA; 9.
SMART; SM00001; EGF_11ke; 3.
SMART; SM000159; PTX; 1.
SMART; SM00327; VWA; 1.
                 Q9YBN2
Q9YBN2;
Q1-NOV-1999
Q1-NOV-1999
Q1-MAR-2002
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Hypothetical
APE1566.
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3567 AA;
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9 (TrEMBLrel. 12, L.
2 (TrEMBLrel. 20, L.
1 protein APE1566.
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                                                          PRELIMINARY;
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69.2%;
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                  Last annotation update)
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                           Last sequence update)
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O90WV3
Q90WV3;
Q90WV3;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-UN-2002 (TrEMBLrel. 21, Last annotation update)
Fas-binding protein Daxx (Fragment).
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PROSITE: PS00022; EGF_1; UNKNOWN_9.
PROSITE: PS01186; EGF_2; 11.
PROSITE: PS01187; EGF_CA; 6.
PROSITE: PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                STRAIN=129SVJ;
ROWEN L., Qin S., Madan A., Loretz C., James R., Dors M., Mi Hall J., Lasky S., Hood L.;
"Sequence of the mouse major histocomaptibility locus class
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387391 MW; 8FBA8276E12293E5 CRC64;
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Pred. No.
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1.6e+02;
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Scoring table:

Searched:

Database

654321

Maximum Minimum

BB BB

seq

length:

Post-processing:

Title: Perfect score:

PCT-US92-08558-3
PCT-US92-08558-2
US-08-249-112-1
PCT-US95-06556-1
US-08-768-301-3
US-09-627-6508-8
US-09-436-063C-4
US-09-436-063C-4
US-09-627-6508-10
US-09-627-6508-10
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ALIGNMENTS

US-08-809-802-7 US-08-072-064-9

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Sequence:

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Total number of hits satisfying chosen parameters:
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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        GenCore version 5.1.6 (c) 1993 - 2003 Compugen
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                                           US-08-809-802-11
US-08-417-30A-15
US-08-417-30A-15
US-09-592-891A-11
US-09-592-891A-12
US-09-130-339-1
US-09-130-339-1
US-09-130-339-1
US-09-130-339-1
US-08-544-559-3
US-08-554-659-1
US-08-17-30A-19
US-08-137-614A-3
US-08-137-614A-3
US-08-072-064-2
US-09-072-064-2
US-08-072-064-5
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Sequence 11, Appl
Sequence 15, Appl
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                       ; NAME/KEY: Coding Sequence; LOCATION: 47...1402; OTHER INFORMATION: US-08-809-802-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 1
US-08-809-802-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/08809802 Patent No. 6455276
                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Av.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEO for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,802
FILING DATE: 19-JUN-1997
CLASSIFICATION ATA:
APPLICATION APPLICATION ET/GB95/02323
FILING DATE: 29-SEP-195
ATTORNEY/AGENT INFORMATION:
NAME: Yablonsky, Michael D
REGISTRATION NUMBER: 40,407
REFERENCE/DOCKET NUMBER: 171292
TELECOMMUNICATION THEORMATION:
                                                                                                                                                                                                         TELEX:
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1555 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 732-594-4678
TELEFAX: 732-594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Le Bourdelles, Beatrice
APPLICANT: Whiting, Paul John
TITLE OF INVENTION: HUMAN ALPHA 4 RECEPTOR SUBUNIT
TITLE OF INVENTION: OF THE GABA-A RECEPTOR
NUMBER OF SEQUENCES: 14
                                                                                                          MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
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RESULT 2
US-09-592-891A-13
Sequence 13, Application Patent No. 6329174
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Pred. No. 6.3e-47;
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APPLICANT: Whichel David Tomalski
APPLICANT: Whochel Paul Mary Wingate
TITLE OF INVENTION: Heliothis Glutamate Rece
FILE REFERENCE: A32815 072667.0118
CURRENT APPLICATION UNUBER: US/09/592,891A
CURRENT FILING DATE: 2001-01-22
NUMBER OF SEQ ID NOS: 14
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 13
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LOCATION: (764)...(76
OTHER INFORMATION: n
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                      TCCTTCTGGATCAACATGGATGCTGCCCCTGCCCGTGTGGGCCTGGGCATCACCACCGTG
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Pred. No. 6.9e-45;
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RESULT 3
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                                                                                                      Matches 488;
                                                                                                                      Query Match
Best Local :
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ADDRESSEE: J. MARK HAND - MERCK &
STREET: 126 EAST LINCOLN AVENUE -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                 FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION
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STATE: NJ
COUNTRY: US
ZIP: 07065-0900
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                                                                                                                      Local Similarity
                                                                                                                                                                                            OTHER INFORMATION
                                                                                                                                                                                                           NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0 FILING DATE: 05-APR-1995
                                                                                                                                                                                                                                                                                                                                   ENGTH:
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APPLICANT: Xiao-Zhou marcha-
APPLICANT: Xavier Georges Sarda
APPLICANT: Michael David Tomalski
APPLICANT: Winchel David Tomalski
APPLICANT: Vincent Paul Mary Wingate
TITLE OF INVENTION: Heliothis Glutamate Receptor
                                                                                                                                 Sequence 11, Application US/09592891A Patent No. 6329174 GENERAL INFORMATION:
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LENGTH: 1609
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Best Local :
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SOFTWARE: FastSEQ fo:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/592,891A CURRENT FILING DATE: 2001-01-22
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ORGANISM: Artificial Sequence
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54.2%;
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Pred. No. 1.5e-43;
0; Mismatches 349;
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US-08-435-933-5
US-08-435-933-5
; Sequence 5, Application
; Sequence 1, Seguence 5, Application
; Patent No. 5693492
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (908) 594-3905
TELEPAX: (908) 594-4720
INPORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3958 base pairs
TYPB: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 0/00 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/M8-DOS
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REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
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NAME: Wallen, III John W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Liu, Ken K.
TITLE OF INVENTION: DNA ENCO
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                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 53. les 473; Conservative
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                   GTGACCACGGACAACAAGTTACTGCGCATCTTCAAGAATGGGAATGTGCTGTACAGCATC
                                                                       AACCGCGTGTGGATGCCCGATCTTTTCTTCTCGAACGAGAAGGAGGGACACTTCCACAAC
                                                                                             GACTCTATCTGGAAGCCAGACCTCTTCTTTGCTAATGAGAAAGGGGCCAACTTCCATGAG
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Pred. No. 1.4e-42;
0; Mismatches 360;
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                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application PC/TUS9605035
GENERAL INFORMATION:
APPLICANT: Cully, Doris F.
APPLICANT: Arena, Joseph P.
APPLICANT: Paress, Philip S.
APPLICANT: Liu, Ken K.
TITLE OF INVENTION: DNA ENCODING GLUTAMATE GATED CHLORIDE TITLE OF INVENTION: CHANNELS
NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
 CLASSIFICATION:
ATTORNEY_AGENT INFORMATION:
NAME: Glesser, Jody M.
REGISTRATION NUMBER: 32,838
REFERENCE_LOCKET NUMBER: 1926
TELECOMMUNICATION INFORMATION:
                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                          STREET: 126 E
CITY: Rahway
STATE: New Je
                                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 07065-0907
                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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126 East Lincoln Avenue
                                                                                                                               PCT/US96/06035
                    19264 PCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA
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Local Similarity 53.7%;
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GCTGCCTTGCTGGAGTATGCTGCCATAAATTTTGTTTCTCG 1073
                                                                        GGCATCACCACCGTGCTCACCATGACCACCCAGAGCTCTGGCTCCCGGGCCTCTTTGCCT
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                                                                                                                                                                                                                     ATCCTGTCCTGGGTCTCCTTCTGGATCAACATGGATGCCCCCTGCCCCGTGTGGGCCCTG
                                                                                                                                                                                                                                                                    TTCAGGCGAGAATTCTCATATTACTTAATACAAATTTATATACCATGCTGTATGTTGGTC
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                                                                                                                           GGTGTCACCACCCTGCTGACCATGGCCACCCAGACGTCGGGCATAAACGCCTCCCTGCCG
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Pred. No. 1.4e-42;
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; OTHER INFORMATION: PCR amplified fragment of Heliothis DNA; OTHER INFORMATION: into pCR2.1-TOPO vector (Invitrogen) US-09-592-891A-12
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SEQ ID NO 12
LENGTH: 1640
TYPE: DNA
ORGANISM: Artificial Sequence
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GATGTACATCCCCAGCCTACTCATCCTCATCCTGGGTCTCCTTCTGGATCAACAT
                                                                                                                                       GTTTATCTTGCGGGATGAGAAGGATCTAGGCTGTTGTACCAAGCACTACAACACAGGGAA
                                                                               ATTCACCTGCATCGAGGTAAAGTTTCACCTGGAACGGCAGATGGGCTACTATCTGATTCA
                                                                                                                 GT---TCACGCTGGAGAAGTTCCTCACTGACTACTGCAACAGTAAGACTAATACCGGTGA
                                                                                                                                                                                  GTTCCTATGGAAGGAAGGCGACC---CGGTGCAGGTGGTGAAAAACTTACACCTGCCTCG
                                                                                                                                                                                                                  GTTTGAGTGGCTGGAAGATGCTCCTGCTGTCCAAGTGGCTGAGGGGGCTGACTCTGCCCCA
                                                                                                                                                                                                                                                                                                              ATACAGTTGCCTGAAGGTAGACCTGCTCTTCAAACGCGAGTTCAGTTACTACCTGATCCA
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; Pred. No. 2.3e:
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2.3e-41;
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; TYPE: DNA
; ORGANISM: ctenocephalides felis
US-09-130-339-1
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Best Local Similarity
Matches 453; Conserv
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APPLICANT: Paress, Philip S.
APPLICANT: Warmke, Jeffrey W.
APPLICANT: Etter, Adrian
APPLICANT: Etter, Adrian
APPLICANT: Brochu, Richard M.
APPLICANT: Brochu, Richard M.
APPLICANT: Brochu, Richard M.
APPLICANT: Brochu, Filard G.
TITLE OF INVENTION: DNA MOLECULES ENCODING CTENOCEPHALIDES
TITLE OF INVENTION: FELIS GLUTAMATE GATED CHLORIDE CHANNELS
FILE REFERENCE: 20029
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CURRENT FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 8
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                                                                                                                        459 TCCTTACGGTTCCGTACTATACAGCATCAGGATATCGCTTACTTTGGCGTGTCCTATGAA
                                                                                                                                                                                                        405 TAATGAGAAAGGGGCCAACTTCCATGAGGTGACCACGGACAACAAGTTACTGCGCATCTT
     585 ACTCTGCAGCCCTCTGCCATCTCTGTCACTTTCAGTTGGCTACACCATGAAAGACCTCGT
                                                        519 TCTGAAACTGTATCCGCTCGATAGGCAGGTGTGCTCTCCCGGATGGCCAGTTA-----
                                                                                                                                         339 TTTAAAATACTTAACACTAACCGAAGCAAGTCGTGTATGGATGCCCGATTTGTTCTTTGC
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Pred. No. 1.4e-39;
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Query Match 9.8%; Score 161.2; DB 4; Length 1297; Best Local Similarity 53.9%; Pred. No. 1.4e-37; Matches 433; Conservative 0; Mismatches 323; Indels 48; Gaps 3; Oy 267 AATGGACTACCGGGTGAATGTCTTCTGCGGCAACAGTGGAATGACCCACGCCTGTCCTA 326 1 1 1 1 1 1 1 1 1 1	TITLE OF INVENTION: DAM MOLECULES ENCODING CTENOCEPHALIDES TITLE OF INVENTION: FELIS GLUTAMATE GATED CHLORIDE CHANNELS FILE REFERENCE: 20029 CURRENT APPLICATION NUMBER: US/09/130,339 CURRENT FILING DATE: 1998-08-06 NUMBER OF SEQ ID NOS: 8 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 3 LENGTH: 1297 TYPE: DNA ORGANISM: Ctenocephalides felis US-09-130-339-3	3 3Applicat 3Applicat 3AST701 3RMATION Cully, I Cully, I Paress, Warmke, Warmke, Etter, A	1055 TGTTTC 1070 1011 CGCCTC 1016	Db 891 GACCGGAGTCTGCCTCCACGTTCGGGGGCTTTGCTCGAATATCGCCCTCGTCAACTA 1010 B91 GACCGGAGTCTGCTCTTTCGGGGGCTTTGCTTGAATATCGCCCTCGTTCAAATTT 1064	OY 885 GGATGCTGCCCCTGCCCGTGTGGGCCTGGGCATCACCACCACCACCACCACCACCACCACCACCACCACC	Oy 765 ATTCACCTGCATCGAGGTAAAGTTTCACCTGGAACGGCAGATGGGCTACTATCTGATTCA 824	1111 111 111 1111 1111 111 1111 1111 1111 1111 1111 1111 1111 1111 1111	Db 573596 OV 645 GTTTGAGTGGCTGGAAGATGCTCCTGCTGCTGCTGCTGAGGGCTGACGGGCTGACTCTGCCCCA 704
laza .	RESULT 10 US-08-554-659-3 Sequence 3, Application US/08554659 Patent No. 5767261 GENERAL INFORMATION: APPLICANT: Wingate, Vincent APPLICANT: Wolff, Mark TITLE OF INVENTION: LEPIDOPTERAN GABA GATED CHLORIDE CHANNEL TITLE OF INVENTION: AND METHODS OF USE THEREOF NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS: ADDRESSE: Scully, Scott, Murphy & Presser	Oy 927 GCTCACCATGACCACGAGGCTCTGGCTCCGGGCCTCTTTGCCTAAGGTGTCCTACGT 986	867 CTCCTTCTGGATCAACATGGATGCTGCCCCTGCCCGTGTGGGCCTGGGCATCACCACCGT	Db 622 CADARACCAPTACCGGTGAATACAGTTGCCTGAAGGTCGACCTGCTCTTTAAACGAGAGTT 681 Qy 807 GGCTACTGATTCAGATTGAACATTCCCCAGCCTACTCATCGTCTCCTGCGT 866	Qy . 687 GGGGCTGACTCTGCCCCCAGTTTATCTTGCGGGATGAGAAGGATCTAGGCTGTTGTACCAA 746	Qy 567 GCTTGAGAGCTCATCCATACTCTGCAGCCCTCTGCCATCTCTGTCACTTTCAGTTGGCTA 626		Db 310 GCCCGATTTGTTCTTTTGCGAATGAAAAGGAGGGCCACTTTCACAACATCATCATGCCGAA 369

ATTORNEY/AGENT INFORMATION:

DiGiglio, Frank

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TELEFAX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1657 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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Best Local Similarity
Matches 474; Conserv
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                              TCCAAGTGGCTGAGGGGCTGACTCTGCCCCAGTTTATCTTGCGGGATGAGAAGGATCTAG
TCCTGTCCTGGGTCTCCTTCTGGATCAACATGGATGCTGCCCCTGCCCGTGTGGGCCCTGG
                                                                    TGGAACGGCAGATGGGCTACTATCTGATTCAGATGTACATCCCCAGCCTACTCATCGTCA 853
                                                                                                     CCATGGAGATTTCTC---TTACGACAGGAAACTACTCTCGTCTGGCATGTGAAATTCAAT 853
                                                                                                                                       GCTGTTGTACCAAGCACTACAACACAGGGAAATTCACCTGCATCGAGGTAAAGTTTCACC
                                                                                                                                                                          TGGGTGTGTCGAGCGAAGTGTCTTTGCCGCAATTCAAGGTGCTGGGCCACCGGCAGCGGG
                                                                                                                                                                                                                                              -----TTGGCTACACCATGCGGGACATCCGATACAAGTGGAATGAGGGGGCCCAACTCAG
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                                                                                                                                                                                                                                                                                                                     TATGCAATATTGAAATCGAAAGTT
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                                                                                                                                                                                                                                                                                                                                                                                      GACTGACTATCACCGCTTCTTGTCCGATGGATTTGCAGTATTTTCCGATGGACCGTCAAT 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTACTACAAGCAACGAATTCATACGCATTCATCATCTGGATCTATTACTAGGAGTATAA
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                                  TTGTAGGCTCGATGGGATACTATTTAATTCAGATTTATATTCCGTCTGGCCTAATTGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                       GGCTGACCCTCATTTTGTCCTGCCTGATGGACCTCAAGAACTTCCCCCATGGACATCCAGA 553
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(516) 742-4366
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                                                                                                      Query Match
Best Local Similarity
                                                                                         Matches 474;
                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: Bloom, Allen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
ZIP: 08
                                                                                                                                                                   NAME/KEY: Coding LOCATION: 104...
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CLASSIFICATION:
                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Dechert Price & Rhoads STREET: 997 Lenox Drive, Building
                                                                                                                                                                                                                                                                           LENGTH:
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                                                        ATTTCCTAGACAAACTTATGGGGCGAACATCTGGATATGATGCCAGGATTCGGCCCAATT
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TTAAAAGGCCCACCCGTGAACGTGACCTGCAACATCTTCATCAACAGTTTCAGCTCCGTCA
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                                                                                      Score 157.8; DB 4;
Pred. No. 1.7e-36;
0: Mismatches 397;
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RESULT 12
US-08-417-330A-19
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NAME: HAND, MARK
REGISTRATION UMBER: 36,545
REFERENCE/DOCKET NUMBER: T110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3905
TELEFAX: 908-594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/
FILING DATE: 05-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1866 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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CITY: RAHWAY
STATE: NJ
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Pred. No. 4.3e-36;
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US-08-554-659-1
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Patent No. 5767261
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GENERAL INFORMATION:
APPLICANT: Wingate, Vincent
APPLICANT: Wolff, Mark
TITLE OF INVENTION: LEPIDOPTERAN GABA GATED CHLORIDE CHANNEL
TITLE OF INVENTION: AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 12
                                                                                                                                                                  APPLICATION NUMBER: US/08/554,61
FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9732
                                                                                        TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                          ZIP: 11530-0299

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Scully, S
                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1657 base pairs
TYPE: nucleic acid
                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Garden City
STATE: New York
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                         STRANDEDNESS:
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                                         CTGCCTTGCTGGAGTATGC 1052
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                      CCAGTTTACTAGAATATGC
                                                                                AGATCTCATATGTCAAGTCCATCGATGTCTATCTGGGAACTTGTTTCGTCATGGTCTTCA 1093
                                                                                                           Conservative
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Pred. No. 4.6e-36;
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: LOCATION: 27...I3
; OTHER INFORMATION:
US-08-417-330A-17
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                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                        Matches
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: WHITING, PAUL
APPLICANT: WINGROVE, PETER
TITLE OF INVENTION: STABLY TRANSFECTED CELL LINE EXPRESSING
TITLE OF INVENTION: GABA-A RECEPTOR AND NOVEL CLONED
TITLE OF INVENTION: GABA-RECEPTOR SUBUNIT CDNA SEQUENCES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 908-594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: HAND, MARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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CITY: RAHWAY
STATE: NJ
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                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Coding Sequence LOCATION: 27...1385
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STRANDEDNESS: doub
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/417,330A FILING DATE: 05-APR-1995
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ZIP: 07065-0900
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   CTGAGTCTGAATAATTTGATGGTCAGTAAAATCTGGACGCCTGACACCTTTTTCAGAAAT
                                   CTGGACCTCGATCCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCTTTGCTAAT
                                                                      TTTTTCGCCAGACCTGGACTGAGAGGGTTGAAGTTTGGGGGGG----CCAACTGAGATT
                                                                                                       TTCTTGCGGCAACAGTGGAATGACCCACGCCTGTCCTACCGAGAATATCCTGATGACTCT
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Pred. No. 4.7e-36;
0; Mismatches 398;
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                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09002361 Patent No. 6329516 GENERAL INFORMATION:
                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert F
OPERATING SYSTEM: DOS
SOFTWARE: FASTSED for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/002.
                                                                                     COUNTRY: USA
ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                    APPLICANT: Halling, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                        COMPUTER:
                                                                                                                                                             STATE:
                                                                                                                                                                           CITY: Lawrenceville
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997 Lenox Drive, Building 3, Suite
                                                                                                                                                                                                                                                                                                    Halling,
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    NAME/KEY: Coding Sequence:
    LOCATION: 2...667
    OTHER INFORMATION:
    US-09-002-361-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX:
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 669 base pairs
LENGTH: 6610 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 8.9%;
Best Local Similarity 54.6%;
Matches 367; Conservative
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NAME: Bloom, Allen
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 669 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                       399 CTTTGCTAATGAGAAAGGGGCCAACTTCCATGAGGTGACCACCGGACAACAAGTTACTGCG
                  999 CATCTGGATGGCTGTGTGTCTCTTTTĞTGTTTCGCTGCCTTGCTGGAGTATGCTGCCAT 1058
                                                                             496
                                                                                                  939 CACCCAGAGCTCTGGCTCCCGGGCCTCTTTGCCTAAGGTGTCCTACGTGAAGGCAATCGA 998
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                                                                                                                                                                                                                                                           GATTCAGATGTACATCCCCAGCCTACTCATCCTCGTCCTGTCCTGGGTCTCCTTCTGGAT
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TGTGTACCTCGGCACCTGCTTCGTTATGGTGTTCACCAGTCTGCTAGAGTACGCGACGGT
                                                                           CACGCTCATGTCTTCCACTAATGCGGCGCTGCCGAAGATCTCGTACGTTAAGTCCATCGA
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Pred. No. 1.9e-33;
0; Mismatches 260;
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Qy 1059 AAATTTTGTTTC 1070
| | | | | | |
Db 616 GGGGTATATGTC 627

Search completed: June 30, 2003, 23:02:26 Job time: $116\ secs$

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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      Published_Applications_Na:*

1: /cgn2_6/ptodata/2/pubpna/U;

2: /cgn2_6/ptodata/2/pubpna/U;

3: /cgn2_6/ptodata/2/pubpna/U;

4: /cgn2_6/ptodata/2/pubpna/U;

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6: /cgn2_6/ptodata/2/pubpna/U;

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9: /cgn2_6/ptodata/2/pubpna/U;

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17: /cgn2_6/ptodata/2/pubpna/U;

18: /cgn2_6/ptodata/2/pubpna/U;

19: /cgn2_6/ptodata/2/pubpna/U;

10: /cgn2_6/ptodata/2/pubpna/U;
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length: 2000000000
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1640
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: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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152 151.6	153.4	155	162.6	162.6	167	168.6	171.8	174.2	181.6	187	187.6	193	219	480.6	807.8	1524.8	1640	Score	
9 9 2 3	9.4	9.5	9.9	9.9	10.2	10.3	10.5	10.6	11.1	11.4	11.4	11.8	13.4	29.3	49.3	93.0	100.0	Match) œ
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US-10-239-420-13 US-09-864-761-5998	US-09-899-495-19	US-09-864-761-11304	US-09-808-483-9	US-09-808-483-11	US-10-239-420-1	US-09-815-925-10	US-10-239-420-3	US-09-969-844-12	US-09-969-844-11	US-09-969-844-13	US-10-239-420-10	US-10-211-673-11	US-09-918-995-15843	US-10-075-846-5	US-10-075-846-9	US-10-075-846-1	US-10-075-846-3	ID	
Sequence 13, Appl Sequence 5998, Ap	Sequence 19, Appl	Sequence 11304, A	Sequence 9, Appli	Sequence 11, Appl	Sequence 1, Appli	Sequence 10, Appl	Sequence 3, Appli	Sequence 12, Appl	Sequence 11, Appl	Sequence 13, Appl	Sequence 10, Appl	Sequence 11, Appl	Sequence 15843, A	Sequence 5, Appli	Sequence 9, Appli	Sequence 1, Appli	Sequence 3, Appli	Description	

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
125.8	127		128.6	130					136.2			136.2	137			137		<u></u>	137	138		138		143.2
7.7	7.7	7.7	7.8							8.3			8.4	8.4	8.4	8.4	8.4	8.4		8.5				8.7
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Sequence 1, Appli	Sequence 5, Appli	Sequence 1, Appli	Sequence 28002, A	Sequence 96, Appl	Sequence, 131, App	Sequence 8, Appli	Sequence 331, App	Sequence 1, Appli	Sequence 1, Appli	Sequence 7, Appli	Sequence 3, Appli	Sequence 9, Appli	Sequence 75, Appl		Sequence 2031, Ap	Sequence 38, Appl	Sequence 38, Appl	œ	-	Sequence 7, Appli	 Sequence 3, Appli 	Sequence 5, Appli	Sequence 6, Appli	Sequence 256, App

ALIGNMENTS

US-10-075-846-3

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; TYPE: DNA
; ORCANISM: homo sapiens
; FEATURE:
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; LOCATION: (1)..(1293)
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                                                                                                                                                                                                                                                                           Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 1640; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.0 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL GLYCINE RECEPTOR ALPHA SUBUNI
TITLE OF INVENTION: IN THE GASTROINTESTINAL TRACT, HGRA4, and SPLICE VARIANT THER
FILE REFERENCE: D0079 NP
CURRENT APPLICATION NUMBER: US/10/075,846
CURRENT FILING DATE: 2002-02-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/269,535 PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1640
                     181
                                                       121
                                                                           121 CCCATGTCCCCCTCTGATTTCCTAGACAAACTTATGGGGCGAACATCTGGATATGATGCC 180
                                                                                                                               61 GTCCTCCTCAGGGTGGCCTTGGCAAAAGAGGGAAGTCAAATCTGGAACCAAGGGGTCCCAG
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GGAGGTCCAATGGAAGGTTCTGGCATTTATAGTCCCCAACCTCCAGCCCCCTCTTCTAAGG
                                                             GTAAAGTTTCACCTGGAACGGCAGATGGGCTACTATCTGATTCAGATGTACATCCCCAGC
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                                                                                             GTCCTCCTCAGGGTGGCCTTGGCAAAAGAGGAAGTCAAATCTGGAACCAAGGGGTCCCAG
                                                                                                      GTCCTCCTCAGGGTGGCCTTGGCAAAAGAGAGTCAAATCTGGAACCAAGGGGTCCCAG
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                                                                                                                                                                   93.0%;
                                                                                                                                                          Score 1524.8;
Pred. No. 0;
0; Mismatches
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Length

Gaps

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120 60 60

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RESULT 2

US-10-075-846-1

Sequence 1, Application US/10075846

Publication No. US20030032608A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A N

TITLE OF INVENTION: IN THE GASTROINTESTINAL TRA

FILE REFERNCE: DD079 NP

CURRENT APPLICATION NUMBER: US/10/075,846

CURRENT FILING DATE: 2002-02-13

PRIOR APPLICATION NUMBER: US 60/269,535

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 81

SOFTWARE: Patentin version 3.0

SEQ ID NO 1

SEQ ID NO 1

LENGTH: 2565

TYPE: DNA

ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                   GTTTGGACAGTTCCTTCCTGATCTCCCACTCAGAACTTCAACTACCAGTCCCAAAGCTAT
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Db 361 CAGTGG		
Qy 301 CAGTGG!	279 CGGGCTGTCTCCCTTTCACTTTCCTCATCTTCATATATCTTCTACTGGGTTGTCTATAAA	B
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Db 241 AGTTTC	GAAGGAGAAACCACGCGGAAACTCTAACGTGGACTGAGGGAGAGAGA	Q
Qy 241 AGTTTC!	1201 OGNOGI CANIOGNANGSI KINGKARIITATAGI CEKAKUUTUU KAGUUCUTUTIAAGG 1250 	당 5
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61	1081 AAAGAATTCATACGACTTCGAAGAAGGCAGAGGCGCCAACGCTTGGAGGAAGATATCATC 1140	Qy
61	979 CTCTTTGTGTTCGCTGCCTTGCTGGAGTATGCTGCCATAAATTTTGTTTTCTCGTCAGCAT 1038	DЬ
Db 1 ATGACAA	1021 CTCTTTGTGTTTCGCTGCCTTGCTGGAGTATGCTGCCATAAATTTTGTTTCTCGTCAGCAT 1080	Qy
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Query Match Best Local Similari	901 CUTGTGGGCCTGGGCATCACCACCGTGCTCACCATGACCACCAGAGCTCTGGCTCCCGG 960	B 4
; ORGANISM: homo sa US-10-075-846-9	CTACTCATCGTCATCCTGTCCTGGGTCTCCTTCTGGATCAACATGGATGCTGCCCCTGCC	D D
; LENGTH: 993 ; TYPE: DNA	CTACTCATCGTCATCCTGTCCTGGGTCTCCTTCTGGATCAACATGGATGCTGCCCCTGCC	Q
; NOMBER OF SEQ ID F ; SOFTWARE: PatentIr ; SEO ID NO 9	739 GTAAAGTTTCACCTGGAACGGCAGATGGGCTACTATCTGATTCAGATGTACATCCCCAGC 798	Дb
	781 GTAAAGTTTCACCTGGAACGGCAGATGGGCTACTATCTGATTCAGATGTACATCCCCAGC '840	Qy
CURRENT APPLICATION COURRENT FILING DATE		망
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US-10-075-846-9 ; Sequence 9, Applica	TTGGCTACACCATGAAAGACCTCGTGTTTGAGTGGCTGGAA	Db .
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Db 1579 TA 1580		Db .
Qy 1621 TA 1622	co.	νQ
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Qy 1561 GTGGGCC	481 CTGTACAGCATCAGGCTGACCCTCATTTTGTCCTGCCTGATGGACCTCAAGAACTTCCCC 540	Q
Db 1459 GTTTGG		Db
Qy 1501 GTTTGG!		νQ
Db 1399 GCTGCTC		망
Qy 1441 GCTGCTC	CCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCTTTGCTAATGAGAAAGGGGCC	Оy
Db 1339 GTGCTAC	301 CAGTGGAATGACCCACGCCTGTCCTACCGAGAATATCCTGATGACTCTCTGGACCTCGAT 360	B &
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ITON: POLYNUCLEOTIDES ENCODING A
PION: IN THE GASTROINTESTINAL TI
DO079 NP
ATION NUMBER: US/10/075,846
DATE: 2002-02-13
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E: 2001-02-16
NOS: 81
                                         -----AGACTACCGGGTGAATGTCTTCTTGCGGCAA
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1.9e-253;
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Sequence 5, Application US/10075846

Publication No. US20030032608A1

REMERAL INFORMATION:
REPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: IN THE GASTROINTESTINAL TRACT, HGRA4, and SPLICE VARIANT THEREOF FILE REFERENCE: D0079 NP
CURRENT APPLICATION NUMBER: US/10/075,846
CURRENT FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: US 60/269,535
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 81
SOCTWARE: Patentin version 3.0
SEQ ID NO 5
LENGTH: 679
TYPE: DNA
ORGANISM: homo sapiens
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                                 Matches 483;
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1118 AACGCTTGGAGGAAGATATCATCCAAGAAAGTCGTTTCTATTTCCGTGGCTATGGCTTTGG
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                                  Conservative
                                             29.3%;
99.2%;
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                                  0;
                                Score 480.6; DB 9; Pred. No. 1.9e-146; 0; Mismatches 4;
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US-09-918-995-15843
; Sequence 15843, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
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, NAME/KEY: misc_feature

; LOCATION: (1)...(492)

; OTHER INFORMATION: n = A,T,C

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Best Local S
Matches 219
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NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 15843
LENGTH: 492
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                              APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SET ITILE OF INVENTION: FROM VARIOUS CDNA LII FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
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                                                                                                            y match 13.4%; Local Similarity 100.0%; res 219; Conservative (
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  TCCCACTCAGAACTTCAACTACCAGTCCCAAAGCTATGTGGGCCTATATTGCATGGTGCC
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                                                                                                                  Score 219; DB; Pred. No. 6.8:0; Mismatches
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4714 ORMATION: S IPTION: S 11.8%; 53.3%; vative CTTATGGG	TELEX: <unknown> INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS: LENGTH: 1555 base pairs TYPE: nucleic acid STRANDEDIESS: single TOPOLOGY: linear MOLECULE TYPE: cDNA FEATURE: NAME/KEY: Coding Sequence</unknown>	PRIOR APPLICATION: <unknown> PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/GB95/02323 FILING DATE: 29-SEP-1995 ATTORNEY/AGENT INFORMATION: NAME: Xu, Yang REGISTRATION NUMBER: 45,243 REFERENCE/DOCKET NUMBER: T1292 TELECOMMUNICATION INFORMATION: TELEPHONE: 732-594-1307 TELEPHONE: 732-594-4720</unknown>	ENGE ADDRE SSSEE Merch STE P.O. BOJ Rahway EN J O7065-0900 READABLE FOI M TYPE: DIC YEADABLE FOI M TYPE: DIC YEADABLE FOI M TYPE: DIC YEADABLE FOI PLICATION NUMING COTION NUMING	RESULT 6 US-10-211-673-11 : Sequence 11, Application US/10211673 : Publication No. US20030013158A1 : Publication No. US20030013158A1 : GENERAL INFORMATION: : APPLICANT: Le Bourdelles, Beatrice : Whiting, Paul John : TITLE OF INVENTION: HUMAN ALPHA 4 RECEPTOR SUBUNIT : NUMBER OF SEQUENCES: 14	Db 177 TCCCACTCAGAACTTCAACTACCAGTCCCAAAGCTATGTGGGCCCTATATTGCATGGTGCC 236 Oy 1584 AATGGTGGCTGTACTTATAAAGATGGCTTATCTACCCTA 1622
RESULT 7 US-10-239-420-10 Sequence 10, Application US/10239420 Publication No. US20030096984A1 GENERAL IMPORMATION: APPLICANT: Cully, Doris F. APPLICANT: Cully, Doris F. APPLICANT: Cheng, Yingcong TITLE OF INVENTION: CHANNELS ENCODING LIGAND GATED ION TITLE OF INVENTION: CHANNELS FROM DERMACENTOR VARIABILIS FILE REFERENCE: 20629P CURRENT APPLICATION NUMBER: US/10/239,420 CURRENT FILING DATE: 2002-09-23 PRIOR APPLICATION NUMBER: PCT/US01/09956 PRIOR APPLICATION NUMBER: 60/193,935 Db 902 ACGGTGCTGACGATGACCACGGTCATGGTCACGCTCCTCCCTC	Oy 802 CAGATGGGCTACTATCTGATTCAGATGTACATCCCCAGCCTACTCATCCTCATCCTGTCC 861	Qy 562 ATGCAGCTTGAGAGCTCATCCATCCATCACCTCTGCCACTTTCAGTT 621	Qy 382 TGGAAGCCAGACCTCTTCTTTTCTAATGAGAAAGGGCCAACTTCCATGAGGTGACCACG 441 Q	287 GCCAACATGGAGTACACCATGACGGTGTTCCTGCACCAGAGCTGGCGGGACAGCAGCTC 322 TCCTACCGAGAATATCCTGATGACTCTCTGGACCTCGATCCCTCCATGCTGGACCTCTATC 1 1 1 1 1 1 1 1 1 1	

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; SEQ ID NO 10
LENGTH: 1197
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; ORGANISM: Rhipicephalus sanguineus
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TYPE: DNA
ORGANISM: Heliothis
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Sequence 13, Application US/0996984

Publication No. US20020192776A1

GENERAL INFORMATION:
APPLICANT: Xiao-Zhou Michelle Wang
APPLICANT: Xivier Georges Sarda
APPLICANT: Michael David Tomalski
APPLICANT: Vincent Paul Mary Wingate
TITLE OF INVENTION: Heliothis Glutamate Receptor
FILE REFERENCE: A32815-1 072667 0.178

CURRENT APPLICATION NUMBER: US/09/969,844

CURRENT FILING DATE: 2001-10-03

NUMBER OF SEQ ID NOS: 14

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 13 AAGTTACTGCGCATCTTCAAGAATGGGAATGTGCTGTACAGCATCAGGCTGACCCTCATT CCAGACCTCTTCTTTGCTAATGAGAAAGGGGCCAACTTCCATGAGGTGACCACGGACAAC ATGGACTACCGGGTGAATGTCTTCTTGCGGCAACAGTGGAATGACCCACGCCTGTCCTAC GGCTACTATCTGATTCAGATGTACATCCCCAGCCTACTCATCGTCATCCTGTCCTGGGTC CACTACAACACAGGGAAATTCACCTGCATCGAGGTAAAGTTTCACCTGGAACGGCAGATG GGGCTGACTCTGCCCCAGTTTATCTTGCGGGATGAGAAGGATCTAGGCTGTTGTACCAAG ACCACAGACGACTTAGTGTTCCTATGGAAGGAAGGCGACC---CGGTGCAGGTGGTGAAN ACCATGAAAGACCTCGTGTTTGAGTGGCTGGAAGATGCTCCTGCTGTCCAAGTGGCTGAG CTTGAGAGCTCATCCATACTCTGCAGCCCTCTGCCATCTCTGTCACTTTCAGTTGGCTAC GTGTACATCCGGATCTTCCCCAACGGCAACGTGCTGTACAGCATCCGAATCTCCTTGACG CCTGATCTATTCTCCCAACGAGAAGGAAGGTCATTTCCACAACATCATCATGCCGAAC AATAATCTTGGAGGTCGCCTCAAATACCTGACACTGACCGAAGCCAACAGAGTCTGGATG ATGGAATACTCCGTACAGTTAACGTTTCGGGAACAATGGTTAGATGAACGGCTCAAATTC CCAGCGGTAGTGAGCGTCAATATATTTGTCCGAAGTATATCAAAGATCGATGACGTCACA CCCGTGAACGTGACCTGCAACATCTTCATCAACAGTTTCAGCTCCGTCACCAAGACCACA TCCTTCTGGATCAACATGGATGCTGCCCCTGCCCGTGTGGGGCCTGGGGCATCACCACCGTG AAGACTAATACCGGTGAATACAGTTGCCTGAAGGTAGACTTGCTCTTCAAACGCGAGTTC ATGGCTAGTT-----ATGGTTGG TTGTCCTGCCTGATGGACCTCAAGAACTTCCCCATGGACATCCAGACGTGCACGATGCAG CGAGAATATCCTGATGACTCTCGGACCTCGATCCCTCCATGCTGGACTCTATCTGGAAG AGTTACTACCTGATCCAGATCTACATTCCGTGCTGCATGCTGGTCATCGTGTCCTGGGTG AACTTACACCTGCCTCGGTTCAC---GCTGGAGAAGTTCCTCACTGACTACTGCAACAGT 0, Score 187; DB 9; 1 Pred. No. 8.2e-50; 0; Mismatches 346; ģ 유 O Length 4621; Indels 48; Gaps

447

569 507 629

567 689

707 687 764 747 821

941

389 327 449

387

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APPLICANT: X140-Zhou Michelle Wang
APPLICANT: Xavier Georges Sarda
APPLICANT: Wichael David Tomalski
APPLICANT: Vincent Paul Mary Wingate
TITLE OF INVENTION: Heliothis Glutamate Receptor
FILE REFERENCE: A32815-1 072667 0178
CURRENT APPLICATION NUMBER: US/09/969,844
CURRENT FILING DATE: 2001-10-03
NUMBER OF SEO ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEO ID NO 11
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: OTHER INFORMATION: PCR amplified fragment of Heliothis DNA cloned:
: OTHER INFORMATION: into pCR2.1-TOPO vector (Invitrogen)
US-09-969-844-11
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TYPE: DNA
ORGANISM: Artificial
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Local Similarity 54.2%;
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ACCATGAAAGACCTCGTGTTTGAGTGGCTGGAAGATGCTCCTGCTGTCCAAGTGGCTGAG
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                                                                                             CTTGAGAGCTCATCCCATACTCTGCAGCCCTCTGCCATCTCTGTCACTTTCAGTTGGCTAC
                                                                                                                                   Conservative
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Pred. No. 2.5e-48;
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Publication No. US20020192776A1

GENERAL INFORMATION:
APPLICANT: Xiao-Zhou Michelle Wang
APPLICANT: Xiao-Zhou Michelle Wang
APPLICANT: Winchell David Tomalski
APPLICANT: Vincent Paul Mary Wingate
TITLE OF INVENTION: Heliothis Glutamate Receptor
FILE REFERENCE: A32815-I 072667.0178

CURRENT APPLICATION NUMBER: US/09/969,844

CURRENT APPLICATION 2001-10-03
                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: PCR amplified fragment of Heliothis DNA cloned
; OTHER INFORMATION: into pCR2.1-TOPO vector (Invitrogen)
US-09-969-844-12
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US-09-969-844-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version SEQ ID NO 12
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 458; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 16
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                CAACATCTTCATCAACAGTTTCAGCTCCGTCACCAAGACCACAATGGACTACCGGGTGAA 284
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                                                                                                                                   ATTAACGTTTCGGGAACAATGGTTAGATGAACGGCTCAAATTCAATAATCTTGGAGGTCG 416
                                                                                                                                                         TGTCTTGCGGCAACAGTGGAATGACCCACGCCTGTCCTACCGAGAATATCCTGATGA 344
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                                                       CCTCAAATACCTGACACTGACTGAAGCCAACAGAGTCTGGATGCCTGATCTATTCTTCTC
                                                                                             CTCTCTGGACCTCGATCCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCTTTGC 404
                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                      10.6%;
                                                                                                                                                                                                                                                                                    Score 174.2; DB 9;
Pred. No. 6.7e-46;
0; Mismatches 343;
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Indels Length

48;

Gaps

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; NAME/KEY: CDS
; LOCATION: (32)...(1225)
US-10-239-420-3
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US-10-239-420-3
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/10239420 Publication No. US20030096984A1 GENERAL INFORMATION:
                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/USO1/09956
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: 60/193,935
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 3
                                                                                                                                                                                                                                                                         APPLICANT: CUILLY, DOTIS F.
APPLICANT: Zheng, Yingcong
TITLE OF INVENTION: DNA MOLECULES ENCODING LIGAND GATED IC
TITLE OF INVENTION: CHANNELS FROM DERMACENTOR VARIABILIS
TILE REFERENCE: 206296
CURRENT APPLICATION NUMBER: US/10/239,420
CURRENT FILING DATE: 2002-09-23
                                                                        TYPE: DNA ORGANISM: Dermacentor variabilis
                                                          FEATURE:
                                                                                                                    LENGTH: 3442
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    RESULT 12
US-09-815-925-10
US-09-815-925-10
: Sequence 10, Application US,
; Patent No. US20020127199A1
; GENERAL INFORMATION:
    APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
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Best Local Similarity
Matches 454; Conserv
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Pred. No. 6.5e-45;
0; Mismatches 357;
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US-09-815-925-10
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SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 10
LENGTH: 1467
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Best Local Similarity
Matches 474; Conserv
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CURRENT FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
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APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: WO. US20020127199Alel Nucleic Acids
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 787CIP2H
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CCTCGACTGTCACTGAGCTTTCGGTTGAAGAGGAACATTGGATACTTCATTCTTCAGACT
                                                                                                                                                                   GAGTGGCTGGAAGATGCTCCTGCTGTCCAAGTGGCTGAGGGGGCTGACTCTGCCCCCAGTTT
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                               ACCTGCATCGAGGTAAAGTTTCACCTGGAACGGCAGATGGGCTACTATCTGATTCAGATG
                                                                                                   ATCTTGCGGGATGAGAAGGATCTAGGCTGTTGTACCAAGCACTACAACACAGGGAAATTC
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                                                                 -TCTCCATCGTGGAGCACCGTCTGGTCTCGAGGAATGTTGTCTTCGCCACAGGTGCCTAT
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Pred. No. 4.3e-44;
0; Mismatches 379;
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LENGTH: 3598
TYPE: DNA
ORGANISM: Dermacentor variabilis
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                                                                                                                                                                                                                                                                                                                                  Matches 451;
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Best Local Similarity
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TITLE OF INVENTION: DNA MOLECULES ENCODING LIGAND GATED ION
TITLE OF INVENTION: CHANNELS FROM DERMACENTOR VARIABILIS
FILE REFERENCE: 20629P
CURRENT APPLICATION NUMBER: US/10/239,420
CURRENT FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: PCT/US01/09956
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-03-28
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PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version
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NAME/KEY: CDS
LOCATION: (170)...(1363)
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                                                                                 382 TGGAAGCCAGACCTCTTTGCTTAATGAGAAAGGGGCCAACTTCCATGAGGTGACCACG
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CCTAATGTACTGGTCCGCGTTAACCCCGAACGGAAAGATTCTATACATGCTCAGGCTCAAG
                                                                                                                                 ACGAGCCCCAACGTATCCAGGCCCCTGGACCTCAATGATCCAAAGCTGGTGCAGCGTATA
                                                                                                                                                              TCCTACCGAGAATATCCTGATGACTCTCTGGACCTCGATCCCTCCATGCTGGACTCTATC
                                                                TGGAAACCGGAAGTATTCTTCGCAAATGCCAAACACGCAGAGTTCCAATATGTCACAGTA
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Pred. No. 2.5e-43;
0; Mismatches 360
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; NAME/KEY: CDS
; LOCATION: (1)..(1455)
US-09-808-483-11
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                                                                                                     Best Loc
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Patent No. US20020001824A1
GENERAL INFORMATION:
APPLICANT: Bayer Aktiengesellschaft
TITLE OF INVENTION: Ligand-gated anion
FILE REFERENCE: Le A 34 397
                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: DE 100 136 19.2 PRIOR FILING DATE: 2001-03-18 NUMBER OF SEQ ID NOS: 18 SOUTWARE: PATENTIN VET. 2.1 EQ ID NO 11
                                                                                                                                                                                                                                                                                             SOFTWARE: PA
                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/808,483
CURRENT FILING DATE: 2001-03-14
                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Drosophila
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TCTTCATCAACAGTTTCAGCTCCGTCACCAAGACCACAATGGACTACCGGGTGAATGTCT
                                 GTTACGACAAGATGAGACCGCCGAAGAAAGAGGGTCAGCCGACGATAGTCTACTTCCATG
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                                                                                                  Score 162.6; DB 10; Pred. No. 3.9e-42; 0; Mismatches 379;
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US-09-808-483-9

; Sequence 9, Application US/09808483

; Patent No. US20020001824A1

; GENERAL INFORMATION:
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                                            APPLICANT: Bayer Aktiengesellschaft
TITLE OF INVENTION: Ligand-gated anion ch
FILE REFERENCE: Le A 34 397
CURRENT APPLICATION NUMBER: US/09/808,483
CURRENT FILING DATE: 2001-03-14
            PRIOR APPLICATION NUMBER: DE 100 136 19.2 PRIOR FILING DATE: 2000-03-18
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Best Local Similarity 52.3%;
Matches 471; Conservative
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TYPE: DNA
ORGANISM: Drosophila melanogaster
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                                                                    GCTCTGGCTCCCGGGCCTCTTTGCCTAAGGTGTCCTACGTGAAGGCAATCGACATCTGGA 1006
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                                                      ACGCCAAATCGCAGTCGTCTTTGCCACCTGTTTCCTATCTCAAGGCAGTGGACGCCTTTA
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Qy 1067 T 1067 Db 968 T 968

Search completed: June 30, 2003, 23:06:59 Job time: 269 secs

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Result
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Listing first 45 summaries
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    401.8
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em_gss_pro:*
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BG404477 602420604
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AUTHORS
TITLE
JOURNAL
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LOCUS
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13483 HSC3DG1	8	14	0		32.	ü
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G196871 RST16	9687	12	0		37.	ö
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G193387 RST1;	9338	12	9		38.	8
G203115 RST22	0311	12	8		38.	27
86166 RST50	8616	12	5	٠	38.	8
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C022502 Homo sap)2250	11	9		21	9
027094 Mus musc	270	11	99	13.4	219.4	8
40664 pg	990	13	S		39.	7

ALIGNMENTS

LOCUS
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AU169868 O1-br-ad cDNA Oryzias latipes cDNA clone br5332, mRNA
Sequence.
ACCESSION
AU169868
VERSION
AU169868.1 G1:12591937
KEYWORDS
EST.
SOURCE
ORGANISM
Oryzias latipes
ELMARYOCAE; Metazoa; Chordata; Craniata; Vertebrata; Euteleostemi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Teleostei; Percomorpha; Acanthomorpha; Acanthopterygii; Teleostei; Percomorpha; Acanthopterygii; Teleostei; Neoteleostei; Neoteleost

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Mus musculus
Eukaryota; Metazoa;
                      house mouse.
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/clone="br5332"
/clone_11b="01-br-ad cDNA"
/sex="female/male mixed"
/tissue_type="brain"
/dev_stage="adult"
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76.4%;
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Pred. No. 2e
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 Craniata; Vertebrata;
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TITLE
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Best Local S
Matches 496
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Mammalia;
1 (bases
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Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10437 row: g column: 01
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National Institutes of Health, Ma
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGATTCAGATGTACATCCCCAGCCTACTCATCGTCATCCTGTCCTGGGTCTCCTTCTGG
                                                                                                                      CAACGCTTGGAGGAAGATATCATCCAAGAAAGTCGTTTCTATTTCCGTGGCTATGGCTTG
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                                           GGCCACTGCCTGCAGGCAAGAGATGGAGGTTCCAATGGAAGGTTCTGGCATTTATAGTCCC
                                                                                          CAGAATAAGGAAGAAGATGTTACTCGTGAAAGTCGTTTTAACTTCAGTGGCTATGGGATG
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(bases 1 to 817)
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/lab_host="0H10B (phage-resistant)"
/lab_host="0H10B (phage-resistant)"
/note="0rgan: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/note="0rgan: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/note="0rgan: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/note="0rgan: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/note="0rgan: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/notI-length clones and constructed by Life Technologies.
/notI-length clones and constructed by Life Technologies.
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/clone="IMAGE:4527768"
/clone_11b="NIH_MGC_94"
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Homo sapiens cDNA HTC clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
Chinese National Human Genome Center at Shanghai
Chinese National Human Genome Center at Shanghai
Chinese National Human Genome Center at Shanghai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
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AV729257 HTC Homo sapiens cDNA clone AV729257
AV729257
AV729257.1 GI:10838678
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70; Conservative
                                                                             CCCACCGGTGAACGTGACCTGCAACATCTTCATCAACAGTTTCAGCTCCGTCACCAAGAC
                                                                                                                        GGACAAGTTAATGGGAAGGACATCAGGATATGATGCAAGAATCAGGCCAAATTTTAAAGG
                                                                                                                                       AGACAAACTTATGGGGCGAACATCTGGATATGATGCCAGGATTCGGCCCCAATTTTAAAGG
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                                                                                                                                                                                    AGACCATGACTCCAGGTCTGGAAAACAACCTTCACAGACCCTATCTCCTTCAGATTTCTT
GACCATGGACTACCGAGTGAATATTTTTCTGAGACAACAGTGGAATGATTCACGGCTGGC
                                                             TCCTCCAGTAAACGTTACTTGCAATATTTTTATCAACAGTTTTGGATCAGTCACAGAAAC
                                                                                                                                                                                                                                                                                                                            199
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clone is available at CHGC in
                                                                                                                                                                                                                                                                                                                            þ
                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HTCCHE03"
/clone_lib="HTC"
                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Hypothalamus"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                        /lab_host="SOLR"
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74.9%;
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Pred. No. 4.3
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AUTHORS
TITLE
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VERSION
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus Ammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus Musculus (bases) 1 to 779)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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http://image.llnl.gov
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/clone_lib="NIH_BNAP_EWO"
/tissue_type="whole brain"
/dev_stage="embryo 15.5 dpc"
/lab_host="phi08 (T] phage resistant)"
lab_host="phi08 (T] phage resistant)
/lab_host="phi08 (T] phi08 
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/db_xref="taxon:10090"
/clone="IMAGE:5708257"
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Email: mEST@mail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
                                                                                                                                                                                                                                                          UI-M-CGOp-bdd-h-07-0-UI.Sl NIH BMAP Ret4 S2 Mus musculus BE981841
                                                                      6001 Executive Blvd. 20892-9643, USA
                                                                                          National Institute
                                                                                                     Contact:
                                                                                                                     97044477
                                                                                                                                            discovery
                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 692)
Bonaldo,M.F., Lennon,G. and So
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70.9%;
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Length

692;

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clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements. The tissue for this library was contributed by Dr. Xin-Yuan Fu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: M13 POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yale University School of Medicine Seq primer: M13 Forward
/clone="UI-M-CGOp-bdd-h-07-0-UI"
/clone=lib="NIH_BMAP_Ret4_S2"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/note="vector: pT739-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_Ret4_S2 library is a subtracted library, ultimately derived from mouse retina tissue libraries at various stages of development. For a detailed description of the library from which this clone was derived, please visit our web site at brainest.eng.ulowa.edu. The tissue for this library was contributed by Dr. Xin-Yuan Fu, Yale University School of Medicine
TAG_SEQ=None found"
190 a 159 c 144 g 198 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="C57BL/6J"
/db_xref="taxon:10090"
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TAATGCAACTTGAAAGCT CCCTCATTTTGTCCTGCCTGATGGACCTCAAGAACTTCCCCATGGACATCCAGACGTGCA CAGATAACAAGCTGCTAAGAATTTTCANAAATGGAAATGTCCTTTATTCAATAAGGTTGA CGGACAACAAGTTACTGCGCATCTTCAAGAATGGGAATGTGCTGTACAGGATCAGGCTGA TGTCCTACCGAGAATATCCTGATGACTCTCTGGACCTCGATCCCTCCATGCTGGACTCTA AGACCACAATGGACTACCGGGTGAATGTCTTCTTGCGGCAACAGTGGAATGACCCACGCC AAGGCCCACCGTGAACGTGACCTGCAACATCTTCATCAACAGTTTTCAGCTCCGTCACCA TTCTGGACAAACTAATGGGGAGGACATCGGGGTATGATGCAAGAATCAGACCCAACTTCA CGATGCAGCTTGAGAGCT TCTGGAAGCCAGACCTCTTCTTTGCTAATGAGAAAGGGGCCAACTTCCATGAGGTGACCA TTGCATACAGTGAATATCCTGACGATTCATTAGACCTTGACCCGTCTATGTTGGATTCCA AAGGTCCTCCAGTTAATGTCACATGCAACATATTCATAAACAGCTTTGGCTCCATTGCAG TGGCCACAAAGGAAACAACAGTGCGCGATCTCGAAGTGCTCCAATGTCACCTTCTGATT TGGCAAAAGAGGAAGTCAAATCTGGAACCAAGGGGTCCCAGCCCATGTCCCCCTCTGATT AGACGACTATGGATTACAGAGTAAACATTTTTCTTCGTCAGAAGTGGAATGATCCTCGTC TCCTAGACAAACTTATGGGGCGAACATCTGGATATGATGCCAGGATTCGGCCCAATTTTA Conservative 669 0; Score 266.6; DB 12; Pred. No. 5.4e-46; 0; Mismatches 145; Indels 0 Gaps 439 379 199 591 499 471 411 319 351 291 231 531 259 0

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351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAS whose availability will be considered under appropriate and limited collaborative arrangements The tissue for this library was contributed by Dr. Xin-Yuan Fu, vale University School of Medicine Seq primer: M13 Forward POLYA-No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6001 Executive Blvd. 20892-9643, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mEST@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 301 443 1706
Fax: 301 443 9890
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6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda,
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Bonaldo, M.F., Lenno
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                   AGACCACAATGGACTACCGGGTGAATGTCTTCTTGCGGCAACAGTGGAATGACCCACGCC
                                                                                                                       AAGGCCCACCCGTGAACGTGACCTGCAACATCTTCATCAACAGTTTCAGCTCCGTCACCA
                                                                                                                                                                 TTCTGGACAAACTAATGGGGAGGACATCGGGGTATGATGCAAGAATCAGACCCAACTTCA
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                                                                              AAGGTCCTCCAGTTAATGTCACATGCAACATATTCATAAAACAGCTTTGGCTCCATTGCAG
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/Clone_lib="NUI_M-COOp-bdc-d-O8-O-UI"
/Clone_lib="NUI_M-COOp-bdc-d-O8-O-UI"
/Clone_lib="NUI_M-COOp-bdc-d-O8-D-O-UI"
/Clone_lib="NUI_M-COOp-bdc-d-O8-D-O-UI"
/Note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_Ret4_S2 library is a subtracted library,
ultimately derived from mouse retina tissue libraries at
various stages of development. For a detailed description
of the library from which this clone was derived, please
visit our web site at brainest.eng.uiowa.edu. The tissue
for this library was contributed by Dr. Xin-Yuan Fu, Yale
University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAG_SEQ=None
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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70.7%;
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Pred. No. 1.3e
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151 g
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BM440664
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VERSION
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   11 Similarity
306; Conser
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Cogburn, L.A. and Nys, Y.
ESTs from Normalized Chicken Reproductive Tract cDNA library-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                       University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-335
Fax: 302-831-2822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BM440664 Linear EST 01-FEB-
pgrln.pk003.m19 Normalized Chicken Reproductive Tract cDNA Libb
(pgrln) Gallus gallus cDNA clone pgrln.pk003.m19 5' similar to
pirlA499701A49970 glycine receptor alpha-4 chain - mouse (fragm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2002)
Contact: Larry A. Cogburn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
   Conservative
                                                                                      85
                                                                                                                                                                                                                                                                                                                                                                                   cogburn@udel.edu, www
Location/Qualifiers
                                                                                 /note-"Vector: pcmvSpoRT6; Library made from three total RNA pools from each tissue (testis 25%, ovary 25%, and oviduct 50% of final RNA pool); Single pass sequencing from 5'-end"
198 c 181 g 88 t
                                                                                                                                                                        and sexually-mature"
/lab_host="E. coli EMDH10B"
                                                                                                                                                                                                                       Library (pgrln)"
/sex="Male and Female"
/tissue_type="Testis, ovary and oviduct"
                                                                                                                                                                                                        /dev_stage="Various stages;embryonic,
                                                                                                                                                                                                                                                                                                              /strain="Commercial broiler
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                 /clone="pgrln.pk003.m19"
                                                                                                                                                                                                                                                                                                                                                    organism="Gallus"
                                                                                                                                                                                                                                                                             'clone_lib="Normalized Chicken Reproductive Tract cDNA
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                   14.6%;
; Score 239.6;
; Pred. No. 2.7e
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                                                                                                                                                                                                                                                                                                                                              gallus"
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GCAACCCTCTCCTTCCTTCTCTCTGGACCCCTGCCAGGGCAGGTCCTCCTCAGGGTGGCC 78

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Series:
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Gunaratne, P.H., García, A.M., Lu, X., Huly
Yoon, V.S., Kowis, C.R., Lawrence, S., Mart
Richards, S., Gibbs, R.A.
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Mus musculus,
                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                   USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (04-APR-2002) National Institutes of Health
Submitted (cotion (MGC), Cancer Genomics Office, Nation
Gene Collection (MGC), Room 11A03, Bethesda, MD
Institute, 31 Center Drive, Room 11A03, Bethesda, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 2991)
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                                                                                                                                                                                                                                                                         Sequencing Center
Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
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                                                           e distribution: MGC clone distribution information can ugh the I.M.A.G.E. Consortium/LLNL at: http://image.llnes: IRAK Plate: 54 Row: .1 Column: 1 clone was selected for full length sequencing because ed the following selection criteria: matched mRNA gi: 1 clone has the following problem: frame shifted.
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:5360070"
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/clone_lib="NIH_MGC_94"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
a 587 c 607 g 920 t
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Email: cgapbs refmail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CINA Library Preparation: Michael J. Brownstein (NHGRI) &

Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human (
Center, Stanford University School of Medicine, Stanford, (
Center, Stanford University School of Medicine, Stanford, (
Web site: http://www-shgc.stanford.edu

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Contact: (Dickson, Mark) mcd@paxil.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 32 Row: b Column: 19 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4504022 This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (01-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens,
BC022502
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CTAATGAGAAAGGGGCCAACTTCCATGAGGTGACCACGGACAACAAGTTACTGCGCATCT
                                                                                                                                                                                   TCTTGCGGCAACAGTGGAATGACCCACGCCTGTCCTACCGAGAATAT-----CCTGATG
                                                                       ACTCTCTGGACCTCGATCCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCTTTG
                                                                                                                                              TCCTGAGACAAAAATGGAATGACCCCAGGTTGAAGCTCCCCAGTGATTTTAGGGGTTCAG
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/note-"Vector: pB
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/db_xref="LocusID:2743"
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/clone_lib="NIH_MGC_96"
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Eutheria;
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SOURCE ORGANISM LOCUS DEFINITION ACCESSION REFERENCE KEYWORDS AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costo,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,F.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. EST BF906462 ILO-OT0123-081200-500-a09 Shotgun sequencing Simpson, A.J BF906462.1 (bases 1 to 536) GI:12297920 of the 536 bp mRNA linear OT0123 Homo sapiens cDNA, human transcriptome with ORF

VERSION

mRNA sequence. EST 18-JAN-2001 BF906462/c

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JOURNAL MEDLINE Laboratory of Cancer Genetics Ludwig Institute for Cancer Re Rua Prof. Antonio Prudente 109 Contact: Simpson A.J.G. Proc. Natl. sequence tags

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Tel: +55-11-2704922 Fax: +55-11-2707001 Brazi

This sequence was Email: asimpson@ludwig derived from the FAPESP/LICR Human

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(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=ILO&t2=ILO-OTO123-
081200-500-a-09&t3=2000-12-08&t4=1)
Seq.primer: puc 18 forward
Seq.primer: puc 18 forward
Eukaryota; Metazoa; Chordata; Cr
Mammalia; Eutheria; Rodentia; Sc
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NIH-MGC http://mgc.nci.nih.gov/.
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
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/db_xref="taxon:10090"

/clone="IMAGE:5367103"

/clone_1lb="NHLMGC_94"

/tissue_type="retina"

/tissue_type="retina"

/lab_host="DH10B (phage-resistant)"

/note="Organ: eye; Vector: pcMV-SPORT6; Site_1: NotI;

/site_2: SalI; Cloned unidirectionally; Oligo-dT primed.

Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies.

Note: this is a NHLMGC Library."

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                   GI:12801693
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                                                                   sapiens
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clone (
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Best Local :
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li, W.B., Gruber, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                      CGATTTATCTGGCAGTCAGGAGATCCTGTGCAATTAGAAAAATTGCCTTGCCTCAATTT
                                                                                                                                                                                                                                                                                                     GACCTCAAGAACTTCCCCATGGACATCCAGACGTGCACGATGCAGCTTGAGAGAGCTCATCC
                                                                                                                                  CAGTTTATCTTGCGGGATGAGAAGGATCTAGGCTGTTGTACCAAGCACTACAACACAGGG
                                                                                                                                                                                                                                                                                      GCTAATGAGAAAGGGGCCAACTTCCCATGAGGTGACCACGGACAACAAGTTACTGCGCATC
                                                                                                                                                                                                  GTGTTTGAGTGGCTGGAAGATGCTCCTGCTGCCAAGTGGCTGAGGGGGCTGACTCTGCCC
                                                                                                                                                                                                                                                        ATACTCTGCAGCCCTCTGCCATCTCTGTCACTTTCAGTTGGCTACACCATGAAAGACCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ummalia; Eutheria;
(bases 1 to 893)
GGGGTCTACGCCCCAACCCTGCTCATTGTTGTTCTCTCCTGGCTTTCCTTCTGGATCAAC
                          CAGATGTACATCCCCAGCCTACTCATCGTCATCCTGGGTCTCCTTCTGGATCAAC
                                                       AACAAMAMADDBKTKGTAGTCATCTTCACCCTGAGGAGGCAGGTCGGCTTTTACATGATG
                                                                                  AAATTCACCTGCATCGAGGTAAAGTTTCACCTGGAACGGCAGATGGGCTACTATCTGATT
                                                                                                                GATATCAAAAAGGAAGATATTGAATATGGTAACTGTACAAAATACTATAAAGGCACGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91006 EVRY cedex - France segref@genoscope.cns.fr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand CDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
188 c 209 g 253 t
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/dev_stage="pooled tissue from
week, 24 week and 26 week)"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 173.2;
Pred. No. 2.3
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ORIGIN
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AUTHORS
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SOURCE
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VERSION
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Query Match
Best Local Similarity 74.4
Matches 229; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov row: e column: 18 High quality sequence stop: 844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 908)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BI825190 908 bp mRNA linear EST 04-OCT-2001 603072067F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5164025 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                      AGAATATCCTGATGACTCTCTGGACCTCGATCCCTCCATGCTGGACTCTATCTGGAAGCC
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                                                                                                    GACTACCGGGTGAATGTC-TTCTTGCGGCAACAGTGGAATGACCCACGCCTGTCCTACCG 329
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  TGAATATCCTGACGACTCTTTAGACCTCGACCCCTCCATGTTGGACTCCATTTGGAAACC
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                                                                                                                                                                                                                                                                                                                                                   341
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                                                                                                                                                                                                                                                                                                                                             /note="organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5164025"
/clone_lib="NIH_MGC_119"
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/lab_host="DH10B"
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Primates;
                                                                                                                                                                                                            Score 171.2; DB 13;
Pred. No. 6e-26;
0; Mismatches 78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwoo, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fj48d02.yl zebrafish adult brain Danio rerio cDNA 5' similar to gb:x52009 GLYCINE RECEPTOR ALPHA-1 CHAIN PRECURSOR (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WashU Zebrafish EST Project 1998
Unpublished (1998)
Other_ESTs: fj48d02.x1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
; Cyprinidae; Danio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: John Ngai. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genom Sequencing Center Clone distribution: Genome Systems, St. Lou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Stephen L. Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     zebrafish
                                                                                                                                                                                                                                                                                                                                                                                                               www.rzpd.de)
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                       114
                                                                                                                                                                                                                                                                                                                                         quality sequence stop: 328
Location/Qualifiers
                                   /note="Vector: pZIPLOX; Site_1: NotI; Site_2: SalI; Original library was constructed in lambdaZIPLOX. A excision of the cDNA library was performed to yield pZIPLOX plasmids. Insert check was done in original library."
                                                                                                                                                                           /sex="mixed male and female"
/tissue_type="brain"
/dev_stage="adult"
                                                                                                                                                                                                                                               /clone_lib="zebrafish adult brain"
                                                                                                                                                                                                                                                                       /organism="Danio rerio"
/db_xref="taxon:7955"
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Ostariophysi; Cypriniformes
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BQ938794
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Best Local Sim
Matches 207;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 CATGTCCCCCTCTGATTTCCTAGACAAACTTATGGGGCGAACATCTGGATATGATGCCAG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            471 GTCCATGCTGGACTCCATCTGGAAACCTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 GATTCGGCCCAATTTTAAAGGCCCACCCGTGAACGTGACCTGCAACATCTTCATCAACAG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BQ938794.1
EST.
                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM13990 row: p column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 975)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5', mRNA sequence.
BQ938794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BQ938794 975
AGENCOURT_8930535 NIH_MGC_94
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                                                                                                                                                                                                                                                                                            High quality sequence stop:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATGTCTCCCTCTGACTTCCTGGATAAACTGATGGGCAGAACGTCCGGCTATGACGCTCG
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      263
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      ω.
/tissue_type="retina"
/lab_host="bHIOB (phage-resistant)"
/lab_host="bHIOB (phage-resistant)"
/note="forgan: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NHLMGC Library."
                                                                                                                                                                   /db_xref="taxon:10090"
/clone="IMAGE:6466531"
/clone_11b="NIH_MGC_94"
                                                                                                                                                                                                                                                        1. .975
                                                                                                                                                                                                                               /organism="Mus musculus"
                                                                                                                                                                                                                                                                       Location/Qualifiers
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Pred. No. 2.4e-25;
Pred. No. 2.4e-25;
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Query Match Best Local S Matches 376

Similarity

9.7%;

Conservative

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Score 159.6; Pred. No. 1.6e 0; Mismatches

1.6e-

Indels Length

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DB 14;

975; 42;

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682	1003	622	943	562	883	502	823	442	763	382	703	322	643	299	583	244	523	184	463	124	403	64	343
réécicarréccrécicircéediriréc 713	TGGATGGCTGTGTGTGTGTTTGTGTTTCGC 1034	GAGTGCACCACCCTCGCAGCCGAGCTTCCTAAAGTGTCTTATGTGAAAGCGCTGGATGTG 681	CAGAGCTCTGGCTCCCGGGCCTCTTTGCCTAAGGTGTCCTACGTGAAGGCAATCGACATC 1002	CCTGATGCTAGTGCTGCCAGAGTACCTCTGGGCATCTTCTCCGTGCTCAGTTTTGGCCTCA 621	ATGGATGCTGCCCCTGCCCGTGTGGGCCTGGGCATCACCACCGTGCTCACCATGACCACC 942	GGCGTATATGCACCAACCTTACTGATTGTGGTTCTCTCTC	CAGATGTACATCCCCAGCCTACTCATCGTCATCCTGTCCTGGGTCTCCTTCTGGATCAAC 882	TACTACACTTGTGTGGAGGTCATCTTCACCCTGAGGAGACAGGTTGGGTTCTACATGATG 501	AAATTCACCTGCATCGAGGTAAAGTTTCACCTGGAACGGCAGATGGGCTACTATCTGATT 822	GATATTAAAAAGGAGATATCGAATATGGCAACTGTACAAAATACTATAAAGGCACTGGT 441	CAGTTTATCTTGCGGGATGAGAAGGATCTAGGCTGTTGTACCAAGCACTACAACACAGGG 762	AGATTCATCTGGCAGTCAGGAGATCCTGTTCAGTTGGAAAAAATTGCTTTACCTCAATTT 381	GTGTTTGAGTGGCTGGAAGATGCTCCTGCTGTCCAAGTGGCTGAGGGGCTGACTCTGCCC 702	TTGGATATACAACCGATGATTTA 321	ATACTCTGCAGCCCTCTGCCATCTCTGTCACTTTCAGTTGGCTACACCATGAAAGACCTC 642	GACTTAACTCTGTTTCCCATGGACACACACACGCTGCAAAATGCAACTTGAGAGCT298	GACCTCAAGAACTTCCCCCATGGACATCCAGACGTGCACGATGCAGCCTTGAGAGCTCATCC 582	TTTCGGGATGGAGACGTCCTTGTGAGCATGAGGTTGTCTATTACACTTTCATGTCCTCTA 243	TTCAAGAATGGGAATGTGCTGTACAGCATCAGGCTGACCCTCATTTTGTCCTGCCTG	GCAAATGAAAAAGTGCCAATTTTCATGATGTGACCCAAGAAATATCCTGTTGTTTATC 183	GCTAATGAGAAAGGGGCCAACTTCCATGAGGTGACCACGGACAAGTTACTGCGCATC 462	GATGCACTGACAGTTGACCCCACCATGTATAAGTGCTTGTGGGAAACCTGACTTATTCTTT 123	GACTCTCTGGACCTCGATCCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCTTT 402

Search completed: June 30, 2003, 23:00:23 Job time : 2198 secs

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AAW97860 AAE13313 AAW05246 ABB65121 AAY51077

> Cat flea glutamate Dermacentor variab

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Title:
Perfect score:
Sequence:
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Maximum
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172186	<pre>/note= "Neurotransmitter-gated ion channel domain"</pre>	44341	/note- "Mature human TRICH-22 protein"	29417	/label= Signal_peptide	128	Location/Qualifiers				muscle disorder; stroke; dementia; anxiety; AIDS; asthma; cirrhosis.	epilepsy; mental disorder; myocarditis; Crohn's disease; Grave's disease;	<pre>chy; amnesia; toxic myopathy; Addison's disease; infection;</pre>	endocrine disorder; autoimmune thyroiditis; rheumatoid arthritis; goitre;	acquired immune deficiency syndrome; immunological disorder; scleroderma;	myasthenia gravis; multiple sclerosis; metabolic disorder; hypertension;	Alzheimer's disease; Parkinson's disease; Huntington's disease; allergy;	cell proliferated disorder; infertility; arteriosclerosis; gene therapy;	depression; schizophrenia; anaemia; Wilson's disease; Cushing's disease;	cardiac disorder; polymyositis; diabetes; neurological disorder; cancer;	amyotrophic lateral sclerosis; cystic fibrosis; neuromuscular disorder;	Human; transporter and ion channel; TRICH-22; transport disorder; angina;		2 protein.		(first entry)			•	AAE21178 standard; Protein; 417 AA.		

Result No.

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Description

SUMMARIES

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R. sanguineus glut
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Dermacentor variab

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CC sclerosis, ataxia telangiectasia, cystlo fibrosis, Becker's muscular dystrophy, diabetes mellitus, diabetes insipidus, myasthenia gravis, compocarditis, prostate cancer, cardiac disorders associated with transport e.g. polymyositis, bradyarrythmia, dermatomyositis, angina, cc neurological disorders associated with transport e.g. amnesia, bipolar cc disorder, depression, Tourette's disorder, schizophrenia, other disorders associated with transport e.g. amnesia, bipolar cc wilson's disease, cattaracts, infertility, hyperglycaemia, hypoglycaemia, cc wilson's disease, cattaracts, infertility, hyperglycaemia, hypoglycaemia, cc wilson's disease, hypercholesterolaemia and cystinuria. Cell croliferated disorders include cancer, actinic keratosis, cirhosis, cc arteriosclerosis, atherosclerosis, birsitis, hepatitis and psoriasis. cc disease, multiple sclerosis, dementia and other extrapyramidal disorder, disease, multiple sclerosis, dementia and other extrapyramidal disorder, system and other developmental disorders of the central nervous system, carriorial cancer, metabolic, endocrine and toxic myopathies, mental disorders, metabolic, anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty, and anyietty and anyietty and anyietty and anyietty and anyietty.
                                                                                                                periodic paralysis, mental disorders including mood, anxiety, and immunological disorders include acquired immune deficiency syndrome (AIDS), adult respiratory distress syndrome, Addison's disease, altergies, asthma, atherosclerosis, osteoporosis, autoimmune haemolytic anaemia, autoimmune thyroiditis, Crohn's disease, atopic dermatitis, crawe's disease, glomerulonephritis, rheumatoid arthritis, scleroderma, systemic lupus erythematosus, systemic sclerosis, ulcerative collitis, haemodialysis, uveitis; viral, bacterial, fungal, parasitic, protozoal, helminthic infections and trauma; and muscle disorders include cardiac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  designated TRICH and nucleic acid molecules encoding such polypeptides. TRICH sequences are useful for diagnosis, treatment and prevention of transport, muscle, neurological, immunological and cell proliferative disorders. Transport disorders include akinesia, amyotrophic lateral sclerosis, ataxia telangiectasia, cystic fibrosis, Becker's muscular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yang J, Yao MG, Lal P, Walia NK, Ğandhi AR, Hafalia AJĀ;
Nguyen DB, Patterson C, Elliott VS, Tribouley CM, Lu DAM, Xu Y;
Reddy R, Hernandez R, Borrowsky ML, Lo TP, Lu Y, Policky JL;
Greene BD, Sanjanwala MS, Raumann BE, Burford N, Ison CH, Lee EA;
Ding L, Das D, Kallick DA, Khan FA, Seilhamer JJ;
                                        myopathy, myocarditis, polymyositis, arrhythmias and TRICH polynucleotides are used in gene therapy. The p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to human transporter and ion channel polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human transporters and ion channels polypeptides and polynucleotides for diagnosing, preventing or treating transport, neurological, muscle, immunological and cell proliferative disorders
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10-AUG-2000;
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25-AUG-2000;
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2000US-226410P.
2000US-228140P.
2000US-230067P.
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K, Gandhi AR,
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Best Local S
Matches 416
                                       Novel nucleic acid sequence encoding human ataxia protein for compounds useful for treating disorders relating to mutations
                                                                          N-PSDB;
                                                                                                          Rappold-Hoerbrand G
                                                                                                                                                                                                                                                                    Human; ataxia; gene therapy
                                                                                                                                                                                                                                                                                                                                                            AAB19336
                                                                                                                                (RAPP/) RAPPOLD-HOERBRAND G.
                                                                                                                                                                            23-MAR-2000; 2000WO-EP02600
                                                                                                                                                                                                   05-OCT-2000
                                                                                                                                                                                                                         WO200058461-A1
                                                                                                                                                                                                                                                                                         Amino acid sequence of a human ataxia protein
                                                                                    2000-656166/63
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        10; Page 20-21; 47pp; English
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                                                                          AAC61678
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                                                                                                                                                                                                                                                                                                                                                          standard; Protein; 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLFVFAALLEYAAINFVSRQH 360
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Pred. No. 1.4e-21
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                                       screening in ataxia
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RESULT 3
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a human ataxia protein. The ataxia protein and polynucleotides are useful for diagnosing and treating disorders related to ataxia. Ataxia gene sequences are useful in gene therapy, and as diagnostic tools or reagents for identifying and characterizing genetic defect involved in the disorders and diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                            WO200188188-A2
                                                                                                                                                                         vasospastic ischaemia;
                                                                                                                                                                                     Mouse; ischaemia;
                                                                                                                                                                                                          Mouse ischaemic condition related protein sequence
                                                                                                                                                                                                                                                         ABB57052
                                                                                                                                                                                                                                                                              ABB57052 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                related to ataxia.
                                 (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON
                                                                               18-MAY-2001;
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                                                                               2001WO-JP04192
                                                       2000JP-0145977
            Asai S,
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                                                                                                                                                                                   compressive ischaemia; occlusive ischaemia;
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             Takahashi Y,
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Pred.
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             Nagata
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5.7e-216;
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                             Brown dog tick; glutamate GluCl2; crop protection;
                                                                                                              R. sanguineus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 LMGRTSGYDARIRPNFKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLSWLSFWINPDASAARVPLGIFSVLSLASECTTLAAELPKVSYVKALDVWLIACLLFGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L-EKIALPQFDIKKEDIEYGNCTKYYKGTGYYTCVEVIFTLRRQVGFYMMGVYAPTLLIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AALLEYAAINFVSROHKEFIRLRRRORR 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAEGLTLPQF-ILRDEKDLGCCTKHY-NTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SITLSCPLDLTLFPMDTQRCKMQLE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSFLLLWTLPGQVLLRVALAKEEVKSGTKGSQ------
                                                                                                                                                                                                                                                                                                                                                                                                                          ASLVEYAVVQVMLNNPK - - - RVEAEKRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LL----VSYDPRIRPNFKGIPVDVVVNIFINSFGSIQETTMDYRVNIFLRQKWNDPRLKLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            496 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                  (first entry)
                                                                                                           glutamate-gated chloride channel 1 protein,
                                                       glutamate-gated chloride channel;
                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.7%; Score 871; DB 2 48.5%; Pred. No. 1e-81;
                                  insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61;
                                                                                                                                                                                                                                                                                 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                  nematocide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -SFGYTTDDLRFIWQSGDP-VQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                  acaricide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PMSPSDFLDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    281
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The invention relates to Rhipicephalus sanguineus (brown dog tick)

2 L-glutamate-gated chloride channel proteins (GluCl1 and GluCl2)

2 and nucleic acid molecules encoding such proteins. GluCl channel

3 proteins are useful for identifying modulators. The compounds

4 identified as modulators are useful for insecticidal, mitacidal

5 and/or nematocidal treatment for use in animal and human health

6 and/or crop protection. The compounds are also useful in screening

7 for and selecting compounds active against parasitic invertebrate

8 species relevant to animal and human health, including worms,

7 fleas, ticks, mites and lice. Heterologous cell lines expressing

7 functional GluCl1 and GluCl2 channel functional forms are useful

8 for establishing functional or binding assays to identify novel

8 GluCl channel modulators. The present sequence is R. sanguineus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GluCl1 protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel L-glutamate-gated chloride channel proteins from Rhipicephalus sanguineus for identifying compounds which modulate the channel proteins, which are useful as insecticides, anthelmintics and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200174838-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Warmke JW, Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MERI ) MERCK & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-OCT-2001
       350
                                                    335
                                                                                                   290
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                                                                                                                                                                                                                                                                                               187
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                                                                                                                                               275
                                                                                                                                                                                                                                             216
                                                                                                                                                                                                                                                                                                                                    156. KNGNVLYSIRLTLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLV
                                                                                                                                                                                                                                                                                                                                                                                          127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD21397
                                                                                                                              QMYIPSLLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDI
                                                                                                                                                                                                                                   FEWLEDAPAVQVAEGLTLPQFIL-RDEKDLGCCTKHYNTGKFTCIEVKFHLERQMGYYLI
WTGVCLTFVFGALLEFALVNYASRSDSRRQNMQKQKQRKWELEPPLDSDHLEDGATTFAM
                                               WMAVCLLFVFAALLEYAAINFVSRQHKEFIRLRRQRRQ-----RLEEDIIQESRFYFRG
                                                                                              QIYIPCCMLVIVSWVSFWLDPTSIPARVSLGVTTLLTMATQISGINASLPPVSYTKAIDV
                                                                                                                                                                                            FLWKEGDP-VQVTKNLHLPRFTLERFQTDY--CTSRTNTGEYSCLRVDLVFKREFSYYLI
                                                                                                                                                                                                                                                                                       PNGDVLFSIRISLVLSCPMNLKFYPLDKQICSI-------VMVSYGYTTEDLV
                                                                                                                                                                                                                                                                                                                                                                                                                                  VFLRQQWNDPRLSYREYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIF 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAIEKRILDSIIGQ-GRYDCRIRPMGINNTDGPAL-VRVNIFVRSIGRIDDVTMEYTVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QPMSPSDFLDKLMGRTSGYDARIRP----NFKGPPVNVTCNIFINSFSSVTKTTMDYRVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VPLVALAFFLLILLSCPSAWAETLPTPPTRGQGGVPVAAAMLLGKQQSSRYQDKEG-KAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VP-ATLSFLLL-----W--TLP-----GQVLLRVALA-----KEEVKSGTKGS
                                                                                                                                                                                                                                                                                                                                                                                     MTFREQWRDERLQYDDLGGQVRYLTLTEPDKLWKPDLFFSNEKEGHFHNIIMPNVLLRIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           517 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-193934P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cully
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ĐĘ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 754.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hamelin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .5e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                      215
                                                                                                                                             334
                                                                                                                                                                                                                                                                                                                                                                                     186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126
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Вb 20 Дb QΥ

104 DPRLSYREYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYS

DERLQYDDLGGQVRYLTLTEPDKLWKPDLFFSNEKEGHFHNIIMPNVLLRIHPNGDVLFS

159 163 99

LDSIIGQ-GRYDCRIRPMGINNTDGPAL-VRVNIFVRSIGRIDDVTMEYTVQMTFREQWR

LDKLMGRTSGYDARIRP----NFKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWN 103

Matches

157;

Conservative

61;

110;

Indels

29;

Gaps

42 48 Local Similarity

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RESULT 5
AAE13037
                                                                        XPPPP
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                   Query Match
Best Local
                                                                                                               Lightamate-gated chloride channel proteins (GluCl and GluCl2) and nucleic acid molecules encoding such proteins. GluCl channel proteins are useful for identifying modulators. The compounds identified as modulators are useful for insecticidal, mitacidal and/or nemarcoidal treatment for use in animal and human health and/or crop protection. The compounds are also useful in screening for and selecting compounds active against parasitic invertebrate species relevant to animal and human health, including worms, fleas, ticks, mites and lice. Heterologous cell lines expressing functional GluCl1 and GluCl2 channel functional forms are useful for establishing functional or binding assays to identify novel GluCl channel modulators. The present sequence is R. sanguineus
                                                                        Sequence
                                                                                                        GluCll protein, T12.
                                                                                                                                                                                                                                                                                                             The invention relates to Rhipicephalus sanguineus (brown dog tick) L-glutamate-gated chloride channel proteins (GluCl1 and GluCl2)
                                                                                                                                                                                                                                                                                                                                                                                                                   Novel L-glutamate-gated chloride channel proteins from Rhipicephalus sanguineus for identifying compounds which modulate the channel proteins, which are useful as insecticides, anthelmintics and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brown dog tick;
                                                                                                                                                                                                                                                                                                                                                                   Claim 26; Fig
                                                                                                                                                                                                                                                                                                                                                                                                       acaricides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-662963/76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-2000; 2000US-193934P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200174838-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhipicephalus sanguineus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluCl2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R. sanguineus glutamate-gated chloride channel 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE13037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE13037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MERI ) MERCK & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-MAR-2001; 2001WO-US09905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C12; crop protection; insecticide; nematocide; acaricide; protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                390 YGLGHCLQARDGGPMEGSGIYS---PQPPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD21395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSSG-----EPAGLMARTWPPPPLP
                                                                        450 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                   2; 89pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glutamate-gated chloride channel; GluCll;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
                   33.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cully DF,
                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            450
Score 742.5; DB : Pred. No. 2.2e-68.
1; Mismatches 11
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                                    DB 22;
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                                    Length 450;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
Query Match
                                                                                              The invention relates to Rhipicephalus sanguineus (brown dog tick) L-glutamate-gated chloride channel proteins (GluCl1 and GluCl2) and nucleic acid molecules encoding such proteins. GluCl channel proteins are useful for identifying modulators. The compounds identified as modulators are useful for insecticidal, mitacidal and/or nematocidal treatment for use in animal and human health and/or crop protection. The compounds are also useful in screening for and selecting compounds active against parasitic invertebrate species relevant to animal and human health, including worms, flore as the parasitic compounds.
                                                                                                                                                                                                                                                                                                      WPI;
                      Sequence
                                           GluCl1 protein, T82.
                                                    species relevant to animal and human health, including worms, fleas, ticks, mites and lice. Heterologous cell lines expressing functional GluCl1 and GluCl2 channel functional forms are useful for establishing functional or binding assays to identify novel gluCl channel modulators. The present sequence is R. sanguineus
                                                                                                                                                                                                             Claim 29; Fig 4; 89pp;
                                                                                                                                                                                                                                           Novel L-glutamate-gated chloride channel proteins from Rhipicephalus sanguineus for identifying compounds which modulate the channel proteins, which are useful as insecticides, anthelmintics and
                                                                                                                                                                                                                                                                                                                         Warmke JW, Yang Y,
                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000; 2000US-193934P
                                                                                                                                                                                                                                                                                                                                                                                             28-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhipicephalus sanguineus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brown dog tick;
GluCl2; crop pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R. sanguineus glutamate-gated chloride channel 1 protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE13038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE13038 standard; Protein; 450 AA.
                                                                                                                                                                                                                                    acaricides
                                                                                                                                                                                                                                                                                                                                                (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T82 protein.
                                                                                                                                                                                                                                                                                                     2001-662963/76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IRLTLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VFAALLEYAAINFVSRQHKEFIRLRRRQRRQ-----RLEEDIIQESRFYFRGYGLGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVIVSWVSFWLDPTSIPARVSLGVTTLLTMATQISGINASLPPVSYTKAIDVWTGVCLTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - VQVTKNLHLPRFTLERFQTDY - - CTSRTNTGEYSCLRVDLVFKREFSYYLIQIYIPCCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IRISLVLSCPMNLKFYPLDKQICSI----
                      450 AA;
                                                                                                                                                                                                                                                                                                                                                                                              2001WO-US09905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ck; glutamate-gated chloride channel;
protection; insecticide; nematocide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                          Cully DF,
33.0%;
                                                                                                                                                                                                              English.
Score
                                                                                                                                                                                                                                                                                                                           Hamelin
742.5;
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В
22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluCl1;
acaricide;
Length 450;
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RESULT 7
AAE16395
ID AAE1
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New nucleic acid encoding lepidopteran chloride screening agents for insecticidal activity -
                                                WPI; 2002-121133/16
N-PSDB; AAD26939.
                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Location/Qualifiers Misc-difference 12..15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE16395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE16395 standard;
                                                                                                                            (AVET ) AVENTIS CROPSCIENCE SA
                                                                                                                                                            13-JUN-2000; 2000US-0592891
                                                                                                                                                                                           13-JUN-2000;
                                                                                                                                                                                                                         11-DEC-2001
                                                                                                                                                                                                                                                         US6329174-B1
                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heliothis virescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lepidopteran glutamate-gated chloride channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heliothis virescens glutamate-gated chloride channel
                                                                                              XM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 DPRLSYREYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYS 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 LDSIIGQ-GRYDCRIRPMGINNTDGPAL-VRVNIFVRSIGRIDDVTMEYTVQMTFREQWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VFAALLEYAAINFVSRQHKEFIRLRRRQRRQ-----RLEEDIIQESRFYFRGYGLGH 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVIVSWVSFWLDPTSIPARVSLGVTTLLTMATQISGINASLPPVSYTKAIDVWTGVCLTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IVILSWVSFWINMDAAPARVGLGITTVLTWTTQSSGSRASLPKVSYVKAIDIWMAVCLLF 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVQVAEGLTLPQFIL-RDEKDLGCCTKHYNTGKFTCIEVKFHLERQMGYYLIQMYIPSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IRLTLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAP 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IRISLVLSCPMNLKFYPLDKQICSI-----VMVSYGYTTEDLVFLWKEGDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DERLQYDDLGGQVRYLTLTEPDKLWKPDLFFSNEKEGHFHNIIMPNVLLRIHPNGDVLFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LDKLMGRTSGYDARIRP----NFKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWN 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -VQVTKNLHLPRFTLERFQTDY--CTSRTNTGEYSCLRVDLVFKREFSYYLIQIYIPCCM
                                                                                              Sarda XG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                           2000US-0592891
                                                                                                                                                                                                                                                                                                 /note-
329
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327
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328
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                                                                                                                                                                                                                                                                                                                                                                                                                    'note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.0%;
                                                                                                Tomalski
                                                                                                                                                                                                                                                                                                                                                                                                                  "Encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                "Encoded by TTGGTGTTGTTA"
                                                                                                                                                                                                                                                                                       "Encoded by
                                                                                                                                                                                                                                                                                                                                                   "Encoded by
                                                                                                                                                                                                                                                                                                                                                                                 "Encoded by TCA'
                                                                                                                                                                                                                                                                                                                     "Encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61;
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                                                                                                                                                                                                                                                                                                                      GCG.
                                                                                                                                                                                                                                                                                                                                                      TTC"
                                                                                                                                                                                                                                                                                                                                                                                                                    AAN"
                                                                                             Wingate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  insecticide
                channel,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                  useful
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                  for
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RESULT 8
AAE16439
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glutamate-gated chloride channel.

Note: This sequence SEQ.ID.NO.14 is stated to be similar to the sequence shown in the sequence listing. However this sequence lacks N-terminal six residues of the sequence shown in sequence listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lepidopteran glutamate-gated chloride channel and this is used, optionally in the form of membrane preparations or recombinant cells, in specific-binding or functional assays for identifying potential insecticides. The present sequence is Heliothis virescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glutamate-gated chloride channel. Glutamate-gated chloride channels are a family of ligand-gated chloride channels unique to invertebrates. The DNA of the invention is used for recombinant production of
Misc-difference
                        Misc-difference
                                                   Misc-difference
                                                                             Misc-difference
                                                                                                        Misc-difference
                                                                                                                                   Misc-difference
                                                                                                                                                                            Heliothis virescens
                                                                                                                                                                                                     Lepidopteran
                                                                                                                                                                                                                              Heliothis virescens glutamate-gated chloride channel, alternative
                                                                                                                                                                                                                                                             09-APR-2002
                                                                                                                                                                                                                                                                                         AAE16439
                                                                                                                                                                                                                                                                                                                  AAE16439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1;
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                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                                                                                    SYTKAIDVWTGVCLTFVFGALLESRFVNYASRSDMHRENMKKARRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTMDYRVNVFLRQQWNDPRLSYREYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTT
                                                                                                                                                                                                                                                                                                                                                                                                           SYVKAIDIWMAVCLLEVFAALLEYAAINFVSR--QHKEFIRLRRRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                        REFSYYLIQIYIPCCMLVIVSWVSFWLDQGAVPARVLLGVTTLLTMATQSSGINASLPPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GWTTDDLVFLWKEGDP-VQVVKNLHLPRFTL--EKFLTDYCNSKTNTGEYSCLKVDLLFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRDEKDL-GCCTKHYNTGKFTCIEVKFHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNKLLRIFKNGNYLYSIRLTLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VTMEYSVQLTFREQWLDERLKFNNLGGRLKYLTLTEANRVWMPDLFFSNEKEGHFHNIIM 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ECMNGGKINFREKEKQILDQILG-PGRYDARIRPSGINGTDGPAVVSVNIFVRSISKIDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVKSGTKGSQPMSPSDFLDKLMGRTSGYDARIRP - - - NFKGPPVNVTCNIFINSFSSVTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Column 14; 18pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PNVYIRIFPNGNVLYSIRISLTLSCPMNLKLYPLDKQTCSLRM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         444 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                     glutamate-gated
                                                                                                                                                                                                                                                            (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    relates
                                                  /note=
286
                                                                             /note=
213
                         333
                                                                                                        /note= "Encoded 18..21
                                                                                                                                                Location/Qualifiers
                                      'note-
                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.7%;
45.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to nucleic acid
                                                                                        "Encoded by TTGGTGTTGTTA"
                                   "Encoded by
           "Encoded
                                                               "Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53;
                                                                                                                                                                                                                                                                                                                 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 737; DB 23;
Pred. No. 8.2e-68;
                                                                                                                                                                                                     chloride channel;
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                                                               AAN"
           TTC"
                                      TCA"
                                                                                                                      ATG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoding lepidopteran
                                                                                                                                                                                                     insecticide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                   347
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RESULT 9
AAE13312
ID AAE1
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AC AAE1

standard;

Protein;

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AAE13312 AAE13312

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Best Local 9
                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                               glutamate-gated chioride channel, alternative form. Note: This sequence SEQ.ID.NO.14 is stated to be similar to the sequence shown in column 14 of the specification. However this sequence contains six additional residues at the N-terminal end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glutamate-gated chloride channel. Glutamate-gated chloride channels are a family of ligand-gated chloride channels unique to invertebrates. The DNA of the invention is used for recombinant production of lepidopteran glutamate-gated chloride channel and this is used, optionally in the form of membrane preparations or recombinant cells, in specific binding or functional assays for identifying potential insecticides. The present sequence is Heliothis virescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Column 27-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding lepidopteran chloride channel, useful screening agents for insecticidal activity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
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                         327
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                                                                                                                                                                                                                                         88 TIMDYRVNVFLRQQWNDPRLSYREYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTT
                                                                                                                                                                                                                                                                            26
                                                                                                                                                                                                                                                                                                                                             Similarity
SYVKAIDIWMAVCLLEVEAALLEYAAINEVSR--QHKEFIRLRRRQ
                                                                  RQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKV
                                                                                                          GWTTDDLVFLWKEGDP-VQVVKNLHLPRFTL--EKFLTDYCNSKTNTGEYSCLKVDLLFK
                                                                                                                                    GYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRDEKDL-GCCTKHYNTGKFTCIEVKFHLE
                                                                                                                                                                                                                        VTMEYSVQLTFREQWLDERLKFNNLGGRLKYLTLTEANRVWMPDLFFSNEKEGHFHNIIM
                                                                                                                                                                                                                                                                            ECMNGGKINFREKEKQILDQILG-PGRYDARIRPSGINGTDGPAVVSVNIFVRSISKIDD
                                                                                                                                                                                                                                                                                            EVKSGTKGSQPMSPSDFLDKLMGRTSGYDARIRP---NFKGPPVNVTCNIFINSFSSVTK
                                                     REFSYYLIQIYIPCCMLVIVSWVSFWLDQGAVPARVLLGVTTLLTMATQSSGINASLPPV
                                                                                                                                                                 PNVYIRIFPNGNVLYSIRISLTLSCPMNLKLYPLDKQTCSLRM----
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                                                                                                                                                                                                                                                                                                                                                                                        450 AA;
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                                                                                                                                                                                                                                                                                                                                                32.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SA
                                                                                                                                                                                                                                                                                                                                 Pred. No. 8.36
3; Mismatches
                                                                                                                                                                                                                                                                                                                                             Score 737; DB 23; Pred. No. 8.3e-68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GABA-gated chloride channel proteins. GABA-gated chloride channel proteins exert toxic effects on other ticks or related parasites such as mites. The present sequence is Dermacentor variabilis clone 8 GABA-gated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chloride channel protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 1; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         animals, comprises the Dermacentor variabilis gamma-aminobutyric acid (GABA)-gated chloride channel - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptide useful for preventing or treating tick infestation, humans, dogs, cattle, horses, deer, or other wild or domesticated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MERI ) MERCK & CO INC
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350
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                                                                                                                                                                                                                                                                                                                      MDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTL
                                                  PQF----ILRDEKDLGCCTKHYNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSWV 289
                                                                                                                                                                                                                                                                                                                                                                                                          -DSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRLTLILISCL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRGYDRRVRPNYGGVPVEVGVTMQIISISTVSEVQMDFTSDFYFRQSWRDERLSFQKSPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSGYDARIRPNFKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRLSYREYPD 114
YAAINFVSRQHKEFIRLRRRQRRQRLEEDIIQESRFYFRGYGLGHCLQARDGGPMEGSGI 409
                                                                                                    SFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLFVFAALLE 349
                                                                                                                                                                                                                                                                    MDLRYFPMDRQACTIEIE-------SFGYTMKDIRYRWSDGDTSVRIAKEVEL
                                                                                                                                                                                                                                                                                                                                                                              LESMTVGAEVAERIWVPDTFFANEKSAYFHAATTPNTFLRIGSGGEVFRSIRLTVTASCP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 736; DB 23;
Pred. No. 1.4e-67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       GABA-gated chloride channel proteins. GABA-gated chloride channel proteins exert toxic effects on other ticks or related parasites such as mites. The present sequence is Dermacentor variabilis clone 5 GABA-gated chloride channel protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptide useful for preventing or treating tick infestation, humans, dogs, cattle, horses, deer, or other wild or domesticated animals, comprises the Dermacentor variabilis gamma-aminobutyric ac
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GABA-gated chloride channel; recombinant expressi
                                                                                                                                                                                                                                                                                                                                                                            Sequence
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N-PSDB; AAD22072.
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                                                                                                                                                                                                                                               Score 732; DB 23;
Pred. No. 3.6e-67;
8; Mismatches 111;
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AAX24372). The invention also provides expression vectors, host cells and methods for recombinant production of CfGluCl-1. Also claimed is a method of identifying a compound that modulates GluCl protein activity which comprises: (a) injecting into a host cell solution a population of nucleic acid molecules (NAMS), at least a portion of which encodes a GluCl protein, such that expression of the portion of NAMS results in an active GluCl; (b) adding a test compound into the solution; and (c) measuring host cell membrane current at a holding potential more positive than the reversal potential for chloride. The products and methods can be used to identify GluCl channel modulators which interfere with
                                                                                                                                                                                                                                                                                                                                         This is the full-length amino acid sequence of CfGluCl-1, a new glutamate gated chloride channel of cat flea (Ctenocephalides felis). The sequence was deduced from an isolated CfGluCl-1 cDNA (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated glutamate gated chloride channels
Ctenocephalides felis, used to develop products
parasites, insects, aphids or nematodes
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N-PSDB; AAX24372.
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    extraintestinal stages of the intestinal worms Strongyloides and Trichinella, and ectoparasites such as ticks, fleas, mites, or lice The active compounds are active against biting insects and other dipterous pests that annoy humans, against household pests such as platella sp. (cockroach), Tineola sp. (clothes moth), Solenopsis invicta (imported fire ant), against agricultural pests such as aphids (Acyrthiosiphon sp.), locusts, spider mites, and boll weevil, against insect pests which attack stored grains such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tribolium sp. and Tenebrio sp., and against immature stages of insects living on plant tissue. The compounds are also useful as nematodicides for the control of soil nematodes and plant parasity such as Meloidogyne sp. The products can also be used for the production of antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiparasitic agents and insecticides in human and animal health and crop protection. They can be used against e.g. gastrointestinal parasites of the genera Ancylostoma, Necator, Ascaris, Strongyloides Trichinella, Capillaria, Trichuris or Enterobius, endoparasites e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                     GINASLPPVSYTKAIDVWTGVCLTFVEGALLEFALVNYASRSDMHRENMKKKRRELEQAA
                                                                                                                                          EED 378
                                                                                                        GSRASLPKVSYVKAIDIWMAVCLLFVFAALLEYAAINFVSR--QHKEFIRLRRQRRQRL
                                                                                                                                                                               CIEVKFHLERQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSS
                                                                                                                                                                                                                                         PLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRDEKDL-GCCTKHYNTGKFT
                                                                                                                                                                                                                                                                                           EGHFHNIIMPNVYIRIFPYGSVLYSIRISLTLACPMNLKLYPLDRQVCSLRM------
                                                                                                                                                                                                                                                                                                                                                                  LRSISEIDDYKMEYSVQLTFREQWQDERLKFNDFGGRLKYLTLTEASRVWMPDLFFANEK
                                                                                                                                                                                                                                                                                                                                                                                                       INSFSSVTKTTMDYRVNVFLRQQWNDPRLSYREYPDDSLDLDPSMLDSIWKPDLFFANEK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RVALAKEEVKSGTKGSQPMSPSDFLDKLMGRTSGYDARIRPN----FKGPPVNVTCNIF
                                                                                                                                                                                                                    ----ASYGWTTNDLVFLWKEGDP-VQVVKNLHLPRFTL--EKFLTDYCNSKTNTGEYS
                                                                                                                                                                                                                                                                                                                                                                                                                                            RLGGGKENFRAKEK-----QVLDQILG-PGHYDARIRPSGVNGTGDGPTV-VAVNIY 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            455 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The GluCl channel modulators can be used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 731.5; DB:
Pred. No. 3.2e-67
0; Mismatches 11:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or Onchocerca,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
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RESULT 12 ·
AAE13313
                                                           AAE13313 standard; Protein;
                                            12-FEB-2002
                                                    AAE13313;
                                           (first entry)
                                                            537
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Dermacentor variabilis clone 9 GABA-gated chloride channel protein.

Gamma-aminobutyric acid; GABAGABA-gated chloride channel; acid; GABA; tick infestation; mite; antiparasitic; e channel; recombinant expression; domestic animal.

Dermacentor variabilis

WO200174884-A1

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RESULT 13
AAW05246
ID AAW05
XX
AC AAW05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to gamma-aminobutyric acid (GABA)-gated chloride channels and their corresponding nucleic acid molecules. GABA-gated chloride channel proteins and DNA's are useful for preventing and treating tick infestation, particularly in humans, dogs, cattle, horses, deer, or other wild or domesticated animals. The nucleic acids are useful as hybridisation probes or Polymerase Chain Reaction primers for identifying the presence of Dermacentor variabilis GABA-gated chloride channel nucleic acid or DNA's encoding for a GABA receptor. The nucleic acids are also useful for the recombinant expression of D. variabilis GABA-gated chloride channel proteins. GABA-gated chloride channel proteins GABA-gated chloride channel proteins. The present sequence is Dermacentor variabilis clone 9 GABA-gated chloride parasites such as mites. The present sequence is Dermacentor variabilis clone 9 GABA-gated chloride parasites such as the channel protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polypeptide useful for preventing or treating tick infestation, in humans, dogs, cattle, horses, deer, or other wild or domesticated animals, comprises the Dermacentor variabilis gamma-aminobutyric acid (GABA)-gated chloride channel -
                                AAW05246 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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   AAW05246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LESMTVGAEVAERIWVPDTFFANEKSAYFHAATTPNTFLRIGSGGEVFRSIRLTVTASCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSGYDARIRPNFKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRLSYREYPD
                                                                                                                                                        YSPQP----
                                                                                                                                                                                                                                                         channel protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fig 1; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               MDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -DSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRLTLILSCL
                                                                                                                      ASPEVSIVKTVGSCQVCPAAVASQGQ
                                                                                                                                                                                        YAAVGYLGK -- RITMRKTRCQQLAKLAEQHRQ-
                                                                                                                                                                                                                         YAAINFVSRQHKEFIRLRRRQRRQRLEEDIIQESRFYFRGYGLGHCLQARDGGPMEGSGI
                                                                                                                                                                                                                                                                                                                           PQFKVLGHVQKAKEVALTTGNYS--RLVC-EIRF--ARSMGYYLIQIYIPAGLIVVISWV
                                                                                                                                                                                                                                                                                                                                             PQF----ILRDEKDLGCCTKHYNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSWV
                                                                                                                                                                                                                                                                                                                                                                                               MDLRYFPMDRQACTIEIE------SFGYTMKDIRYRWSDGDTSVRIAKEVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRGYDRRVRPNYGGVPVEVGVTMQIISISTVSEVQMDFTSDFYFRQSWRDERLSFQKSPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           537 AA;
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                                   Protein;
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                                                                                                                                                      ----PAPLLREGE
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                                   456 AA
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Best Local S
Matches 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                acid sequence was deduced from a Drosophila head cDNA clone (AAT43596 Recombinant GluCl, or host cells expressing it, can be used to screen for modulators of GluCl that can be used as ectoparasitic, anthelmintic, acaricide or insecticide agents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A novel Drosophila glutamate gated chloride channel (GluCl) (AAW05246) is selectively opened by either avermectin or glutamate and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       binding protein agents for the t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster strain Oregon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiparasitic;
acaricide; inse
                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid encoding Drosophila avermectin and/or glutamate binding protein - useful for isolating cpds. used as antiparasitic agents for the treatment or prevention of helminthiasis in domestic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-506147/50.
N-PSDB; AAT43596.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-MAY-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    represents
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                TCIEVKFHLERQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQS
                                                                                                                                                                                                          FINSFSSVTKTTMDYRVNVFLRQQWNDPRLSYREYPDDSLDLDPSMLDSIWKPDLFFANE
                                                                                                                                                                                                                                                                                         VLLRVALAKEEVKSGTKGSQPMSPSDFLDKLMGRTSGYDARIRP---NFKGPPVNVTCNI
                                                                                                                                                    KGANFHEVTTDNKLLRIFKNGNVLYSIRLTLILSCLMDLKNFPMDIQTCTMQLESSSILC
                                                                                                                                                                                     FVRSIMTISDIKMEYSVQLTFREQWTDERLKFDDIQGRLKYLTLTEANRVWMPDLFFSNE
                                                                                                                                                                                                                                                         ILYFASLCSASLANNAKVNFREKEKKVLDQILG-AGKYDARIRPSGINGTDGPAIVRINL
                                                  ----ASYGWTTNDLVFLWKEGDP-VQVVKNLHLPRFTL--EKFLTDYCNSKTNTGEY
                                                                                SPLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRDEKDL-GCCTKHYNTGKF
                                                                                                                    KEGHFHNIIMPNVYIRIFPNGSVLYSIRISLTLACPMNLKLYPLDRQICSLRM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 45-46; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cully DF,
                                                                                                                                                                                                                                                                                                                                                                                               456
                                                                                                                                                                                                                                                                                                                                                                                                                              plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a target of avermectin action in arthropods. Its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           insecticide;
                                                                                                                                                                                                                                                                                                                             Conservative
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23..456
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                                                                                                                                                                                                                                                                                                                                           32.4%; Score 730.5;
42.3%; Pred. No. 4e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu
Sig_peptide
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                                                                                                                                                                                                                                                                                                                             61;
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Mismatches 120;
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Indels
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one (AAT43596).
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Best Local Similarity
Matches 160; Conser
                                                                                                                                                                                                                     capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryctes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                   Sequence
                                                                                                                                                                        The sequence data for this patent did not form specification, but was obtained in electronic at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 22155; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila; developmental biology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster polypeptide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB65121;
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                                                                                                                                                                                                            (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                             invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                           2001-656860/75
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                        GYDARIRPNEKGPPVNVTCNIFINSESSVTKTTMDYRVNVELRQQWNDPRLSYREYPD-D
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SYDKRVRPNYGGPPVEVGVTMYVLSISSLSEVKMDFTLDFYFRQFWTDPRLAYRKRPGVE
                                                 LPRT-PLLTIW-----LAINMALIAQETGHKRIHTVQAATGGGSMLGDVNISAILDSFSV
                                                                       VPATLSFLLLWTLPGQVLLRVALAKEE-----VKSGTKGSQPMSPSDFLDKLMGRTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGINASLPPVSYTKAIDVWTGVCLTFVFGALLEFALVNYASRSGSNKANMHKENMKKKRR
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2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   PWD,
                                                                                                                                                                                                                                                                                                                                                         detection reagent for detecting for elucidating cell signalling
                                                                                                  83;
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                                                                                                Score 729; DB 22;
Pred. No. 8.8e-67;
3; Mismatches 138
                                                                                                                                                                                                                                                                                                                                                                                                                                  Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell signalling; insecticide;
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                                                                                                                       Length 606;
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RESULT 15
AAY51077
ID AAY51
Drosophila simulans
                                                             GABA receptor; fruitfly; invertek pesticide resistance; GABA-gated
                                                                                                                             D. simulans GABA receptor variant RldMD-RR protein.
                                                                                                                                                                                                                                                              AAY51077 standard;
                                           insecticide; RldMD-RR.
                                                                                                                                                                        22-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLFVFAALLEYA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQ
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                                                                                                                                                                                                                                                                                                                                                                                                              IYSPQPPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TVGYMAK-----RIQMRKQRFMAIQKIAEQKKQQLDGANQQQANPNPNANVGGP-GGVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AINEVSRQHKEFIRLRRRQRRQRLEEDIIQESRFYFRGYGLGHC---LQARDGGPMEGSG 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F----KVLGHRQRAMEISLTTGNYSRLACEIQFVRSMGYYLIQIYIPSGLIVIISWVSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILRDEKDLG----CCTKHYNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSWVSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LQYFPMDRQLCHIEIE-----SFGYTMRDIRYKWNEGPNSVGVSSEVSLPQ
                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                       411
                                                                                                                                                                                                                                                                                                                                                                                                              417
                                                             invertebrate; gamma aminobutyric acid
BA-gated chloride channel; cyclodiene;
                                                                                                                                                                                                                                                              637
                                                             receptor;
insect;
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US6008046-A 02-JUN-1993; 28-DEC-1999 9308-0072064.

Jackson MB, 04-OCT-1991; (-IH4O) OPHIDIAN PHARM Ffrench-Constant 91US-0770881 RH;

XX PF

Purified receptor GABA

N-PSDB;

AAZ44048

2000-086222/07

Example 2; Column 53-56; 51pp; English.

This invention describes novel purified and isolated nucleic acids (I) encoding mutant invertebrate gamma aminobutyric acid (GABA) receptors Expression of the GABA receptor is used for drug and pesticide screening and for identifying GABA antagonists or agonists. The methods allow large numbers of compounds potentially useful as drugs or pesticides to be screened and to find compounds which overcome existing or potential resistance mechanisms e.g. pesticides which are capable of blocking GABA-gated chloride channels resistant to cyclodienes. (I) may be used to detect mutants by the polymerase chain reaction (PCR) and/or hybridization and to detect and genotype insects which may be resistant to insecticides which affect the GABA receptor. Introducing (I) into a

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Best Local S
Matches 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  beneficial insect may render the insect resistant to a pesticide and can be used in combination with pesticides in the field to reduce or eliminate the presence of harmful insects only. The insect GABA receptor shows critical pharmacological differences from the vertebrate receptor which may result in the development of insect-specific insecticides with greater safety for vertebrate exposure. This sequence represents a variant Drosophila simulans (fruitfly) GABA receptor RIdMD-RR described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                               32.2%; Score 726; DB 21; cal Similarity 36.7%; Pred. No. 1.9e-66; 156; Conservative 86: Microschile.
438 GPGGP 442
                           413 QPPAP 417
                                                       385
                                                                                                              325
                                                                                                                          296 DAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLEVFAALLEYAAINF 355
                                                                                                                                                                356 VSROHKEFIRLRRRORRORLEEDIIQESRFYFRGYGLGHC---LQARDGGPMEGSGIYSP 412
                                                                                                                                                                                                                                                                                                                                                   46 LPRT-PLLTIW-----LAINMALIAQETGHKRIHTVQAATGGGSMLGDVNISAILDSFSV
                                                                                                                                                                                                                                                                                                                                                                                                                   5 VPATLSFLLLWTLPGQVLLRVALAKEE-----VKSGTKGSQPMSPSDFLDKLMGRTS 56
                                                     MAK-----RIQMRKQRFMAIQKIAEQKKQQLDGANQQQANPNPNANVGGP-GGVGVGPG 437
                                                                                                           637 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 637;
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Search completed: June 25, 2003, 17:15:32 Job time : 64.6734 secs

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Result
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Perfect score:
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2163
21682.5
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1602.3
1580.5
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678.5
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652.5
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1: /cgn2_6/ptodata/1/pubpaa/us
2: /cgn2_6/ptodata/1/pubpaa/us
3: /cgn2_6/ptodata/1/pubpaa/us
4: /cgn2_6/ptodata/1/pubpaa/us
6: /cgn2_6/ptodata/1/pubpaa/us
6: /cgn2_6/ptodata/1/pubpaa/us
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9: /cgn2_6/ptodata/1/pubpaa/us
11: /cgn2_6/ptodata/1/pubpaa/us
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12: /cgn2_6/ptodata/1/pubpaa/us
13: /cgn2_6/ptodata/1/pubpaa/us
14: /cgn2_6/ptodata/1/pubpaa/us
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length: 2000000000
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2252
1 MTTLVPATLSFLLI
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Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
Listing first 45 summaries
 : /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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:/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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Copyright (c) 1993 - 2003 Compu
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US-10-075-846-13
US-10-075-846-12
US-10-075-846-11
US-10-075-846-11
US-10-075-846-11
US-10-075-846-14
US-09-969-844-14
US-09-960-198-7
US-09-800-198-7
US-09-800-198-7
US-10-239-420-2
US-10-239-420-2
US-10-239-420-3
US-09-910-652A-39
0 US-09-910-652A-39
0 US-09-910-682-39
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1307.255 Million cell updates/sec
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          sequence 13, Appl
Sequence 15, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 39, Appl
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RESULT 1 US-10-075-846-4

ALIGNMENTS

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26.3	26.4	26.4	26.7	26.8	27.0	27.0	27.0	27.3	27.3	27.3		.~	27.3	27.3	27.3	27.3	27.3	27.3	27.4	\sim	27.5			28.1	28.1
466	468	468	345	392	420	467	467	535	485	464	464	464	464	464	464	464	464	464	465	554	465	465	423	422	397
9	10	9	9	9	9	10	9	10	10	10	10	10	10	10	9	9	9	9	9	9	10	9	10	10	10
US-09-839-446-8	US-09-898-570-6	US-09-839-446-6	US-09-765-069-10	US-09-765-069-4	US-09-765-069-8	US-09-742-311-2	US-09-765-069-2	US-09-808-483-10	US-09-808-483-12	US-09-898-570-38	US-09-898-570-37	US-09-898-570-36	US-09-898-570-35	US-09-742-311-4	US-09-839-446-38	US-09-839-446-37	US-09-839-446-36	US-09-839-446-35	US-09-818-657-4	US-10-211-673-8	US-09-893-321-2	US-09-818-657-2	US-09-808-483-8	US-09-808-483-4	US-09-808-483-6
'n	ь Ф	Sequence 6, Appli	10	Sequence 4, Appli	Sequence 8, Appli	Sequence 2, Appli	2, Ap	10,		38,	37,	36,	35	Sequence 4, Appli	Sequence 38, Appl	Sequence 37, Appl	Sequence 36, Appl	ω 5	4	ε •	e 2,	2, 7	Sequence 8, Appli	Sequence 4, Appli	Sequence 6, Appli

Sequence 4, Application US/10075846 Publication No. US20030032608A1 GENERAL INFORMATION: APPLICANT: Bristol-Myers Squibb Company TITLE OF INVENTION: POLYNUCLEOTIDES ENCOING A NOTITE OF INVENTION: IN THE GASTROINTESTINAL TRAFFILE REFERENCE: D0079 NP CURRENT APPLICATION NUMBER: US/10/075,846 CURRENT FILING DATE: 2002-02-13 PRIOR APPLICATION NUMBER: US 60/269,535 PRIOR APPLICATION NUMBER: US 60/269,535 NUMBER OF SEQ ID NOS: 81 SOFTMARE: Patentin version 3.0 SEQ ID NO 4 망 Ş В Ş В Qy 밁 Q ; TYPE: PRT; ORGANISM: homo sapiens US-10-075-846-4 Query Match 100.0%; Best Local Similarity 100.0%; Matches 431; Conservative (LENGTH: 431 181 181 61 61 RIRPNEKGPPVNVTCNIFINSESSVTKTTMDYRVNVFLRQQWNDPRLSYREYPDDSLDLD 120 MDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRD 240 EKDLGCCTKHYNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPA 300 RIRPNFKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRLSYREYPDDSLDLD 0; Score 2252; DB 9; Pred. No. 1.1e-206; Mismatches A NOVEL GLYCINE RECEPTOR ALPHA SUBUNI TRACT, HGRA4, and SPLICE VARIANT THER Length 431; 0 Gaps 60 120

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APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL GLYCINE RECEPTOR ALPHA SUBUNIT
TITLE OF INVENTION: IN THE GASTROINTESTINAL TRACT, HGRA4, and SPLICE VARIANT THEREO
FILE REFERENCE: D0079 NP
CURRENT APPLICATION NUMBER: US/10/075,846
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: US 60/269,535
PRIOR APPLICATION NUMBER: US 60/269,535
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 417
TYPE: PRT
ORGANISM: homo sapiens
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Best Local S
Matches 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                              421
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     407
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                                                                                                                                                                                                                                                                                                                MTTLVPATLSFLLLWTLPGQVLLRVALAKEEVKSGTKGSQPMSPSDFLDKLMGRTSGYDA
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                             EGETTRKLYVD 431
                                                                    KEFIRLRRRQRRQRLEEDIIQESRFYFRGYGLGHCLQARDGGPMEGSGIYSPQPPAPLLR 420
                                                                                                                                                                        EKDLGCCTKHYNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPA
                                                                                                                                                                                                               MDIQTCTMQLE-----SFGYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRD
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                                                                                                                                                           EKDLGCCTKHYNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPA
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     EGETTRKLYVD 417
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Pred. No. 3.4e-198;
0; Mismatches 1;
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                                                                                                     GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL GLYCINE RECEPTOR ALPHA SUBUNI

TITLE OF INVENTION: IN THE GASTROINTESTINAL TRACT, HGRA4, and SPLICE VARIANT THER

FILE REFERENCE: D0079 NP
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US-10-075-846-13
CURRENT APPLICATION NUMBER: US/10/075,846
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: US 60/269,535
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin version 3.0
SEQ ID NO 12
LENGTH: 337
                                                                                                                                                                       Sequence 12, Application US/10075846 Publication No. US20030032608A1
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Matches
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ORGANISM: Homo
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Sequence 13, Application US/10075846
Publication No. US20030032608A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING
TITLE OF INVENTION: IN THE GASTROINTESTINAL
FILE REFERENCE: D0079 N
CURRENT APPLICATION NUMBER: US/10/075,846
CURRENT FILING DATE: 2002-02-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/269,535
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin version 3.0
SEQ ID NO 13
SEQ ID NO 13
SREYERGYGLGHCLQARDGGPMEGSGIYS-PQPPAPLLREGETTRKLYVD 431
||| | |||:|||| :: | ||| ::|: :| :||
SRENESGYGMGHCLQVKDGTAVKATPANPLPQPP----KDGDAIKKKEVD 413
                                                                                           LSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRDEKDLGCCTKHYNTGKFTCIEVK 262
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                                                                                                                                                                                                                                                                                 ---SFGYTMNDLIFEWLSDGP-VQVAEGLTLPQFILKEEKELGYCTKHYNTGKFTCIEVK
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CURRENT APPLICATION NUMBER: US/10/075,846
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: US 60/269,535
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEO ID NOS: 81
SOFTWARE: PatentIn version 3.0
SEQ ID NO 15
SEQ ID NO 15
TYPE: PAT
ORGANISM: homo sapiens
US-10-075-846-15
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US-10-075-846-15
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: LOCATION: (322)..(322)
: OTHER INFORMATION: wherein "X" is any
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Best Local
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TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL GLYCINE RECEPTOR ALPHA SUBUNIT E
TITLE OF INVENTION: IN THE GASTROINTESTINAL TRACT, HGRA4, and SPLICE VARIANT THEREOF
FILE REFERENCE: D0079 NP
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FEATURE:
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                                                                                                                                    PSDFLDKLMGRTSGYDARIRPNFKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWN 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEROMGYYLIOMYIPSLLIVILSWVSFWINMDAAPARVGLGITTVLTMTTOSSGSRASLP
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            IRLTLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAP
                                                                                                                      PSDFLDKLMGRTSGYDARIRPNFKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWN
                                                                   DPRLSYREYPODSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYS
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No. US20030032608A1
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Pred. No. 5.5e-152;
7; Mismatches 7;
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; ORGANISM: Homo
US-10-075-846-11
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RESULT 7
US-10-075-846-10
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US-10-075-846-11
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Publication No. US20030032608A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL GLYCINE RECEPTOR ALPHA SUBUNI
TITLE OF INVENTION: IN THE GASTROINTESTINAL TRACT, HGRA4, and SPLICE VARIANT THER
FILE REFERENCE: D0079 NP
CURRENT APPLICATION NUMBER: US/10/075,846
CURRENT FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: US 60/269,535
PRIOR PRICATION NUMBER: US 60/269,535
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 81
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Best Local Similarity
Matches 312; Conserva
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SEQ ID NO 11
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----SFGYTMNDLIFEWQDEAP-VQVAEGLTLPQFILKEEKDLRYCTKHYNTGKFTCIEV
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                                                                                                                                                           FSSVTKTTMDYRVNVFLRQQWNDPRLSYREYPDDSLDLDPSMLDSIWKPDLFFANEKGAN 141
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73.8%;
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Pred. No. 1.4e-144;
5; Mismatches 43;
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RESULT 8
US-10-075-846-14
Sequence 14, Application US/10075846
Sequence 14, Application US/2003608A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: FOLYNUCLECTIDES ENCODING A STITLE OF INVENTION: IN THE GASTROINTESTINAL TR.
FILE REFERENCE: D0079 NP
CURRENT APPLICATION NUMBER: US/10/075,846
CURRENT FILING DATE: 2002-02-13
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Publication No. US/2003032608A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A I
TITLE OF INVENTION: IN THE GASTROINTESTINAL TRACE
FILE REFERENCE: D0079 NP
CURRENT APPLICATION NUMBER: US/10/075,846
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: US 60/269,535
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
VUMBER OF SEQ ID NOS: 81
SOFTMARE: PATENTIAN VERSION 3.0
SEQ ID NO 10
LENGTH: 449
                 ; TYPE: PRT ; ORGANISM: homo sapiens US-10-075-846-14
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; ORGANISM: Homo
US-10-075-846-10
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                                                               SEQ ID NO 14
LENGTH: 298
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Best Local
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                                                                                              CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: US 60/269,535
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin version 3.0
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307; Conserv
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Pred. No. 1.7e-142;
8; Mismatches 50;
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APPLICANT: Xiao-Zhou Michelle Wang
APPLICANT: Xavier Georges Sarda
APPLICANT: Wichael David Tomalski
APPLICANT: Vincent Paul Mary Wingate
TITLE OF INVENTION: Heliothis Glutamate Receptor
FILE REFERENCE: A32815-I 072667.0178
CURRENT APPLICATION NUMBER: US/09/969.844
CURRENT FILING DATE: 2001-10-03
NUMBER OF SEQ ID NOS: 14
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US-09-969-844-14
US-09-969-844-14
; Publication No. US20020192776A1
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Best Local Similarity
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                                                                                                                                              DNKLLRIFKNGNVLYSIRLTLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSV 207
                                                                                                                                                                                                                                                                                      EVKSGTKGSQPMSPSDFLDKLMGRTSGYDARIRP---NFKGPPVNVTCNIFINSFSSVTK
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REFSYYLIQIYIPCCMLVIVSWVSFWLDQGAVPARVLLGVTTLLTMATQSSGINASLPPV
                                                                                                                               PNVYIRIFPNGNVLYSIRISLTLSCPMNLKLYPLDKQTCSLRM-----
                                                                                                                                                                                              VTMEYSVQLTFREQWLDERLKFNNLGGRLKYLTLTEANRVWMPDLFFSNEKEGHFHNIIM 144
                                                                                                                                                                                                                             TIMDYRVNVFLRQQWNDPRLSYREYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTT 147
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                              RQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKV 326
                                                               GWTTDDLVFLWKEGDP-VQVVKNLHLPRFTL--EKFLTDYCNSKTNTGEYSCLKVDLLFK
                                                                                            GYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRDEKDL-GCCTKHYNTGKFTCIEVKFHLE
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95.2%;
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                                                                                                                                                                                                                                                                                                                             Score 737; DB 9;
Pred. No. 6.7e-62;
3; Mismatches 111
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247 266 Gaps

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RESULT 11
US-09-800-198-74
US-09-800-198-74
Sequence 74, Application US/09800198
Publication No. US20030087816A1
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Best Local S
Matches 146
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PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 87
LENGTH: 533
TYPE: PRT
       GENERAL INFORMATION:
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-09-808-602-87
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CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 09/800,198
PRIOR FILING DATE: 2001-03-05
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APPLICANT: Fernance
APPLICANT: Shimket
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US20020155115A1
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Herrman, John
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Mezes, Peter S
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Pred. No. 1.5e-60;
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US-09-800-198-74
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CURRENT APPLICATION NUMBER: US/10/239,420
CURRENT FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: PCT/US01/09956
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: 60/193,935
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                         RESULT 12
US-10-239-420-2
                                                                                                                                                                                                         Sequence 2, Application US/10239420
Publication No. US20030096984A1
GENERAL INFORMATION:
APPLICANT: Cully, Doris F.
APPLICANT: Zheng, Yingcong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/800,198 · CURRENT FILING DATE: 2001-03-05 PRIOR APPLICATION NUMBER: 60/186,596 PRIOR FILING DATE: 2000-03-03 NUMBER OF SEO ID NOS: 98

SOFTWARE: Patentin Ver. 2.1.
SEO ID NO 74

LENGTH: 533
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Best Local Similarity
Matches 146; Conserv
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                      TITLE OF INVENTION: DNA MOLECULES ENCODING LIGAND TITLE OF INVENTION: CHANNELS FROM DERMACENTOR VAR FILE REFERENCE: 20629P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME FILE REFERENCE: 15966-697
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Mishra, Vishna
Mezes, Peter S
Rastelli, Luca
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; Pred. No. 1.5e-60;
80; Mismatches 122
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LENGTH: 397
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Best Local Similarity
 INFORMATION
                                                                                                                                  APPLICATION NUMBER: PCT/GB95/02323 FILING DATE: 29-SEP-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Le Bourdelles, Beatrice
Whiting, Paul John
TITLE OF INVENTION: HUMAN ALPHA 4 RECEPTOR SUBUNIT
                                                                  REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                         PRIOR APPLICATION DATA:
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TELEX: <Ur
                                                                                                                                                                                                        APPLICATION NUMBER: US/10/211,673 FILING DATE: 02-Aug-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RTTLGVTTLLTISSKGSGIQSNLPPVSYVKAIDVWMGACTGEVESALLEFTVVSCLAR 330
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ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
                                TELEFAX: 732-594-4720
                                                                                                    REGISTRATION NUMBER: 45,243
                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ fo
NT APPLICATION DATA:
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ZIP: 07065-0900
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Pred. No. 2.9e-60;
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US-10-239-420-5
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                                                                                                                                                                               SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 422
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/10239420 Publication No. US20030096984A1 GENERAL INFORMATION:
                                                                                         Query Match
Best Local
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cully, Doris F.
APPLICANT: Zheng, Yingcong
TITLE OF INVENTION: DNA MOLECULES ENCODING LIGAND GATED ION
TITLE OF INVENTION: CHANNELS FROM DERMACENTOR VARIABILIS
FILE REFERENCE: 20629P
                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: 60/1
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/239,420
CURRENT FILING DATE: .2002-09-23
PRIOR APPLICATION NUMBER: PCT/US01/09956
                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 PGQVLLRVALAKEEVKSGTKGSQPMS-----PSDFLDKLMGRTSGYDARIRPNFKGPP
                                 48 LDKLMGRTSGYDARIRP-NFKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 PARLLAPLLLLCAQQLRGTRAMNDIGDYVGSNLEISWLPNLDGLIAGYARNFRPGIGGPP
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RRQRLEEDI 379
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Pred. No. 2.6e
68; Mismatches
                                                                    Score 655; DB 9; I
Pred. No. 4.1e-54;
Pred. No. 4.1e-54;
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF BREAST CANCER
FILE REFERENCE: 20121.491C1
CURRENT APPLICATION NUMBER: US/09/510,662A
CURRENT FILING DATE: 2000-02-22
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 39
SEQ ID NO 39
TYPE: PRT
ORGANISM: Homo sapiens
US-09-510-662A-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Dillon, Davin C. APPLICANT: Day, Craig H. APPLICANT: Wang, Aijun
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273 VSWYSFWLDVDAIPARITLGVTTLLTISSESSDHQANLAPVSYVKALDVWMGTCTMFVFA 332
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                                                                                                                                                                                                  175 DLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLP 234
                                                                                                                                                                                                                                        333 AVLEFTFVSYLARR 346
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327 AHYSSLQQ----MAAKDRGTTKEVEEVSITNIINSSISSFK 363
                                                                                                                    209 QYTI--ERYFTLVTRSQQETGNYTRLVLQFELRRNVLYFILETYVPSTFLVVLSWVSFWI 266
                                                                                                                                                                               163 DLSKYPMDTQTCKLQLE------SWGYDGNDVEFTWLRGNDSVRGLEHLRLA 208
                           353 INFVSRQHKEFIRLRRRQRRQRLEE----DIIQESRFYFR 388
                                                                                                                                                                                                                                                                                                    55 TSGYDARIRPNFKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRLSYRBYPD 114
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Search completed: June 25, 2003, 17:18:50

Job time : 37.6756 secs

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1 MTTLVPATLSFLLL
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      GenCore version 5.1.6 . (c) 1993 - 2003 Compugen Ltd.
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US-08-137-614A-24
US-09-592-891A-14
US-09-130-339-2
US-08-435-933-6
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US-08-072-664-8
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	ery st tch	SEQU LE TY TY TO MOLE 08-137	TELECOMMUNICATION INFORMATION: TELEPHONE: (716)263-1636 TELEFAX: (716)263-1600	ATTORNEY_AGENT INFORMATION: NAME: Timian, Susan J. REGISTRATION NUMBER: 34,10 REFERENCE/DOCKET NUMBER: 1	S = A = S	800	COM	ST	S A	NUN	SENERAL INFORMATION: APPLICANT: Soderlund APPLICANT: Knipple, APPLICANT: Henderson APPLICANT: Henderson	SULT 1 -08-137 Sequence		444	41 42	40 40	36	ω ω ι ω 4 π	32	228
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APPLICANT: Xiao-Zhou Michelle Wang
APPLICANT: Xavier Georges Sarda
APPLICANT: Michael David Tomalski
APPLICANT: Michael David Tomalski
APPLICANT: Vincent Paul Mary Wingate
TITLE OF INVENTION: Heliothis Glutamate Receptor
FILE REFERENCE: A32815 072667.0118
CURRENT APPLICATION NUMBER: US/09/592,891A
CURRENT FILING DATE: 2001-01-22
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 14
LENGTH: 450
TYPE: PRT
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Best Local (
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45.7%; Pred. No. 1.3e-69;
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                                                                                                    GENERAL INFORMATION:
APPLICANT: Cully, Doris F.
APPLICANT: Arena, Joseph P.
APPLICANT: Paress, Philip S.
APPLICANT: Liu, Ken K.
APPLICANT: Liu, Ken K.
TITLE OF INVENTION: DNA ENCODI
TITLE OF INVENTION: CHANNELS
NUMBER OF SEQUENCES: 6
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Matches
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CURRENT FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
                                                                                                                                                                                                                                                      Sequence 6, Application US/08435933 Patent No. 5693492
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APPLICANT: Paress, Philip S.
APPLICANT: Warmke, Jeffrey W.
APPLICANT: Etter, Adrian
APPLICANT: Cohen, Charles J.
APPLICANT: Brochu, Richard M.
APPLICANT: Brochu, Richard M.
APPLICANT: Brochu, Molecules Encoding CTENOCEPHALIDES
TITLE OF INVENTION: FELIS GLUTAMATE GATED CHLORIDE CHANNELS
FILE REFERENCE: 20029
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                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: John W. Wallen III
                                    STREET:
                 STATE:
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Pred. No. 4.9e
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                                                                                                                         Sequence 6, Application PC/TUS9606035
GENERAL INFORMATION:
APPLICANT: Cully, Doris F.
APPLICANT: Arena, Joseph P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                        APPLICANT: Paress, Philip S.
APPLICANT: Liu, Ken K.
TITLE OF INVENTION: DNA ENCODING
TITLE OF INVENTION: CHANNELS
NUMBER OF SEQUENCES: 6
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LENGTH: 456 amino acid
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
              CORRESPONDENCE ADDRESS:
ADDRESSEE: Jody M. Glesser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Wallen, III John W.
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REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 19264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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54; Conservative
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126 East Lincoln Avenue -
                                                                                                       Cully, Doris F.
Arena, Joseph P.
Paress, Philip S.
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                                                                             GLUTAMATE
P.O.
BOX 2000-0907
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RESULT 6
US-09-627-650B-19
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               Sequence 19. Application US/09627650B
Patent NO. 6406872
GEMERRAL INFORMATION:
APPLICANT: Bamber, Bruce
APPLICANT: Jorgensen, Erik
APPLICANT: Jorgensen, Erik
TITLE OF INVENTION: Nematode Neuromuscular Junction
TITLE OF INVENTION: Methods Related Thereto
FILE REFERENCE: 21101.0009U3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 32.4%; Score 730.5; DB Best Local Similarity 42.3%; Pred. No. 6.3e-69
CURRENT APPLICATION NUMBER: US/09/627,650B
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Giesser, Jody M.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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CLASSIFICATION:
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TOPOLOGY: lir
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; OTHER INFORMATION:
; OTHER INFORMATION:
US-09-627-650B-19
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                                                                                                                                                                                                                                                                                                           sequence 8, Application US/08072064
Patent No. 6008046
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PRIOR FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 50
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 19930602
                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                               APPLICANT: FFRENCH-CONSTANT, RICHARD H.
APPLICANT: JACKSON, MEYER B.
TITLE OF INVENTION: DRUG AND PESTICIDE SCREENING
                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                      STREET:
                                             SOFTWARE:
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                                                                                                                                                                       SSEE: PETER G. CARROLL
T: 220 Montgomery Street,
San Francisco
                                                                                                                              94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                          California
                                             PatentIn Release #1.0,
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                                                                                                                                          United States of America
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ER: 09/436,063
              US/08/072,064
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Pred. No. 6.
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                                                                                                                                                                                       Suite
                                               Version
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US-09-002-361-6
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Best Local S
Matches 156
                                                                                                                                                                                   Sequence 6, Application US/09002361
Patent No. 6329516
GENERAL INFORMATION:
APPLICANT: Halling, Blaik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415/397-8338 INFORMATION FOR SEQ ID NO:
                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                   APPLICANT: Halling, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 637 amino acids
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ATTORNEY/AGENT INFORMATION:
   COMPUTER
                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                    CITY:
                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 7 FILING DATE: 04-OCT-1997
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                                 COUNTRY:
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                                                                 Lawrenceville
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READABLE FORM
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                                                                                  E: Dechert Price 997 Lenox Drive,
                                   USA
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Building
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                                                                                    Suite
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US-09-002-361-3
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                                                                                                                                                                Sequence 3, Application US/09002361 Patent No. 6329516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 32.2%; Score 724.5; DB 4; Best Local Similarity 37.8%; Pred. No. 2.7e-68; Matches 153; Conservative 79; Mismatches 120;
                                                                                        GENERAL INFORMATION:
APPLICANT: Halling, Blaik
TITLE OF INVENTION: Lepidopteran GABA-Gated Chloride
TITLE OF INVENTION: Channels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 459 amino acid
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building
CITY: Lawrenceville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,
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SOFTWARE: FastSEQ for
CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
COMPUTER: I
                                                                                                                                                                                                                                                                                                                                           306 VGYMAKRIQMRKQREVAIQKIASEKKIPVDCPPVGDPHTLSKMGTLGRCPPGRPSEVRFK
                                                                                                                                                                                                                                                                                                                                                                                                               191 -----KVLGHRQRAMEISLTTGNYSRLACEIQFVRSMGYYLIQIYIPSGLIVIISWVSFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 QYFPMDRQLCHIEIE------SFGYTMRDIRYKWNEGPNSVGVSSEVSLPQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 KNEPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 LDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRLTLILSCLMDL
                                                                                                                                                                                                                                                                         366 VHDPKAHSKGGTLENTINGGRSGAEEENPGPPPHILHPGKDISKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 YDARIRÞNFKGPPVNYTCNIFINSFSSVTKTTMDYRVNVFLRQQQNDPRLSYREYPD-DS
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FastSEQ for Windows Version
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                    Suite 210
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                                                                                      Sequence 5, Application US/09002361 Patent No. 6329516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
               GENERAL INFORMATION:
APPLICANT: Halling,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 467 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
 NUMBER
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STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                     224 AVQVAEGLTLPQFILRDEKDLG----CCTKHYNTGKFTCIEVKFHLERQMGYYLIQMYIP 279
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                                                                                                                                                                                                                                                                                            LLEVFAALLEYAAINFVSRQHKEFIRLRRRQRRQRLEEDIIQESRFYFRGYGLGHCLQAR 399
                                                                                                                                                                                                 DGPPGSAEPIPPPRTSTLSRPPPP
                                                                                                                                                                                                                                   DGGPMEGSGIYSP-----QPPAP 417
                                                                                                                                                                                                                                                                                                                                           SGLIVIISWVSEWLNRNATPARVSLGVTTVLTMTTLMSSTNAALPKISYVKSIDVYLGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IRLTITASCPMDLQYFPMDRQLCNIEIE------SFGYTMRDIRYKWNEGPN 177
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                                                                                                                                                                                                                                                                                                                                                                             SLLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVC 339
                                                                                                                                                                                                                                                                                                                                                                                                                 SVGVSSEVSLPQF-----KVLGHRQRAMEISLTTGNYSRLACEIQFVRSMGYYLIQIYIP
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 SEQUENCES:
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                                                      Blaik
                  Channels
                                 Lepidopteran GABA-Gated Chloride
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Pred. No. 2.8e-68;
                                                                                                                                                                                                 358
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RESULT 11
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   Sequence 2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: BLOOM, Allen REGISTRATION NUMBER: 29,135 REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite
CITY: Lawrenceville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sir
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                    INMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLFVFAALLEYAA 352
                                                                                                                                                                                                                                                                                                                        ILRDEKDLG----CCTKHYNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSWVSFW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRLTLILSCLMDL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TDKRVRPNYGGPPVEVGVTMYVLSISSVSEVLMDFTLDFYFRQFWTDPRLAYKKRTGVET
 Application US/09002361
                                                                                                                         -----DGGPME------GSGIYSPQPPAPLLREGETTRKL 428
                                                                                                                                                            VGYMAKRIQMRKQRFVAIQKIASEKKIPVDCPPVGDPHTLSKMGTLGRCPPGRPSEVRFK
                                                                                                                                                                                                                                                                                                      ----KVLGHRQRAMEISLTTGNYSRLACEIQFVRSMGYYLIQIYIPSGLIVIISWVSFW
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                                                                                        VHDPKAHSKGGTLENTINGGRSGAEEENPGPPPHILHPGKDISKL 432
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IBM Compatible
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internal
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Matches 152; Conserv
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MOLECULE TYPE:
FRAGMENT TYPE:
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APPLICANT: Halling, Blaik
TITLE OF INVENTION: Lepidopteran GABA-Gated Chloride
TITLE OF INVENTION: Channels
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette
COMPUTER: IBM Compatit
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for
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CLASSIFICATION:
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REFERENCE/DOCKET NUMBER:
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DGGPMEGSGIYSP-----QPPAP
                                                   FVMVFASLLEYATVGYMAK-----RIQMRKQRFTAVQKMAAEKKMQI---
                                                                                                                                         SLLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVC
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997 Lenox Drive, Building 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              609-520-3259
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Gaps

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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEFAX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                      Matches 156;
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDJUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: LEPIDOPTERAN GABA GATED CHLORIDE CHANNEL TITLE OF INVENTION: AND METHODS OF USE THEREOF NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wingate, Vi
APPLICANT: Wolff, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 488 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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    Application US/08554659
    5767261

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11530-0299
                                                                                                                                     AVQVAEGLTLPQFILRDEKDLG----CCTKHYNTGKFTCIEVKFHLERQMGYYLIQMYIP
                                                                                                                                                                                                                                   LLFVFAALLEYAAINFVSRQHKEFIRLRRRQRR----QRLEED---------
                                                                           SLLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVC
                                                                                                                                                                             IRLTITASCPMDLQYFPMDRQLCNIEIE-----
                                                                                                                                                                                                                                                                                              SAILDSL---SVSYDKRVRPNYGGPPVDVGVNMYVLSISSLSEVKMDFTLDFYFRQFWTD
FVMVFTSLLEYATVGYMAK-----RIQMRKQRFTAVQKMQIDGPPGSAEPIPPPRTSTL 375
                                                                                                                   SVGVSSEVSLPQF-----KVLGHRQRAMEISLTTGNYSRLACEIQFVGSMGYYLIQIYIP
                                                                                                                                                                                                       IRLTLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAP
                                                           SGLIVIISWVSFWLNRNATPARVSLGVTTVLTMTTLMSSTNAALPKISYVKSIDVYLGTC
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Pred. No. 9.1e-68;
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                                                                                                                                                                            ---SFGYTMRDIRYKWNEGPN 206
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US-08-554-659-4
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Best Local :
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TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 97:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 488 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                             105 PRLSYREYPD-DSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYS
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                        340 LLFVFAALLEYAAINFVSRQHKEFIRLRRQRR----QRLEED---
                                                                                                                                                                                                              224 AVQVAEGLTLPQFILRDEKDLG-----CCTKHYNTGKFTCIEVKFHLERQMGYYLIQMYIP
                                                                                                                                                                                                                                                                                                                                                      101 PRLAYKKSTGVETLSVGSEFIRNIWVPDTFFVNEKQSYFHIATTSNEFIRIHHSGSITRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                44 SAILDSL---SVSYDKRVRPNYGGPPVDVGVNMYVLSISSLSEVKMDFTLDFYFRQFWTD
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T: 400 Garden City Plaza
Garden City
                                                                      SGLIVIISWVSEWLNRNATPARVALGVTTVLTMTTLMSSTNAALPKISYVKSIDVYLGTC
                                                                                                                  SLLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVC
                                                                                                                                                                SVGVSSEVSLPQF-----KVLGHRQRAMEISLTTGNYSRLACEIQFVGSMGYYLIQIYIP
                                                                                                                                                                                                                                                                                                      IRLTLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAP
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                                                                                                                                                                                                                                                          IRLTITASCPMDLQYFPMDRQLCNIEIE------SFGYTMRDIRYKWNEGPN
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Pred. No. 9.1e-68;
5; Mismatches 106
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FVMVFTSLLEYATVGYMAK-----RIQMRKQRFTAVQKMQIDGPPGSAEPIPPPRTSTL

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US-08-072-064-1

Patent No. 6008046 GENERAL INFORMATION:

Application US/08072064

NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETER G. CARROLL

TITLE OF INVENTION:

JACKSON, MEYER B.

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CHROMOSOME/SEGMENT: III; polytene subregion MAP POSITION: approximately map unit 26
                                                                                                                             100 SYDKRVRPNYGGPPVEVGVTMYVLSISSVSEVLMDFTLDFYFRQFWTDPRLAYRKRPGVE 159
                                                      160 TLSVGSEFIKNIWYPDTFFVNEKQSYFHIATTSNEFIRVHHSGSITRSIRLTITASCPMN
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                                                                                                                                                57 GYDARIRPNEKGPPVNVTCNIFINSESSVTKTTMDYRVNVFLRQQWNDPRLSYREYPD-D 115
                                                                                                                                                                                                                                       5 VPATLSFLLLWTLPGQVLLRVALAKEE------VKSGTKGSQPMSPSDFLDKLMGRTS 56
   LKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQ 235
                                                                                                                                                                                                       LPRT-PLLTIW-----LAINMALIAQETGHKRIHTVQAATGGGSMLGDVNISAILDSFSV 99
                                                                           SIDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRLTLILSCLMD 175
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                                                                                                                                                                                                                                                                                                 32.0%; Score 720; DB 3; Length 637; 36.5%; Pred. No. 1.4e-67;
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US-08-072-064-4
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Patent No. 6008046
                                                                                                                                                Matches
                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: FFRENCH-CONSTAN
APPLICANT: JACKSON, MEYER
                                                                                                                                                                                                                                                                                                                 TELEFAX: 415/397-8338 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 7
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 415/705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: San
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                             LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      385 MAK-----RIQMRKQRFMAIQKIAEQKKQQLDGANQQQANPNPNANVGGP-GGVGVGPG 437
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100 SYDKRVRPNYGGPPVEVGVTMYVLSISSVSEVLMDFTLDFYFRQFWTDPRLAYRKRPGVE 159
               155;
                                                                   46 LPRT-PLLTIW-----LAINMALIAQETGHKRIHTVQAATGGGSMLGDVNISAILDSFSV 99
                                                                                                    5 VPATLSFLLLWTLPGQVLLRVALAKEE-----VKSGTKGSQPMSPSDFLDKLMGRTS
                                                                                                                                                                                                                                                                            AMINO ACID
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220 Montgomery Street,
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                                                                                                                                             Mismatches, 144;
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US-08-072-064-1

Query Match Best Local S Matches 155

Local Similarity nes 155; Conserv

Conservative

TELEFAX: 415/37 1:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 637 amino acids
TYPE: AMINO ACID
TYPE: AMINO ACID

1:

REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPTELECOMMUNICATION INFORMATION:
TELEPHONE: 415/705-8410
TELEPAX: 415/397-8338

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 770,881
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.

CARROLL, PETER G.

CLASSIFICATION: APPLICATION NUMBER: UFILING DATE: 19930602

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:

US/08/072,064

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

Floppy disk

COUNTRY:

94104

STREET:

San Francisco

220 Montgomery Street,

California

United States of America

MOLECULE TYPE: ORIGINAL SOURCE:

peptide

POSITION IN GENOME

ORGANISM:

Drosophila melanogaster

S В

	438 GPGGP 442	43	
	413 QPPAP 417	41	
437	5 MAKRIQMRKQRFMAIQKIAEQKKQQLDGANQQQANPNPNANVGGP-GGVGVGPG 437	385	
412	QHKEFIRLRRRQRRQRLEEDIIQESRFYFRGYGLGHCLQAR	35	
384	325 NATPARVSLGVTTVLTMTTLMSSTNAALPKISYVKSIDVYLGTCEVMVFASLLEYATVGY	32	
355	DAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLFVFAALLEYAAINF	296	
324	FRVLGHRQ-RATEINLTTGNYSRLACEIQFVRSMGYYLIQIYIPSGLIVVISWVSFWLNR 324	266	
295	FILRDEKDLGCCTKHYNTGKFTCIEVKFHLEROMGYYLIOMYIPSLLIVILSWYSFWINM	236	
265	220 LQYFPMDRQLCHIEIESFGYTMRDIRYFWRDGLSSVGMSSEVELPQ 265	22	
235	5 LKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQ 235	176	
219	160 TLSVGSEFIKNIWVPDTFFVNEKQSYFHIATTSNEFIRVHHSGSITRSIRLTITASCPMN 219	16	
175	II6 SUDEDPSMEDSIWEPDLEFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRLTLILSCEMD 175	1.1	

Search completed: June 25, 2003, 17:18:06 Job time : 25.1409 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 2000000000
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Qy 325 Db 287	Qy 265 Db 227	Qy 205 Db 168	Qy 145 Db 121	Qy 85	Qy 25 Db 1	Query Match Best Local Matches 32	A; Residues: 1- A; Cross refere C; Genetics: A; Gene: Gla4 C; Superfamily: C; Keywords: ne	A; Accession: A499/0 A; Status: preliminary; A; Molecule type: DNA	R;Matzenbach, J. Biol. Chem. A;Title: Struc A;Reference nu	3 C S L S	RESULT 1	30 692 31 697.5 32 687.5 33 670.5 35 670.5 36 663.5 37 664.5 38 653.5 40 648.5 41 645.5 42 643.5 43 634.5 634.5 634.5
KVSYVKAIDIWMAVCLLEVFAALLEYAAINFVSRQHKEFIRLRRRQRRQRL 	LEROMGYYLIOMYIPSLLIVILSWVSFWINMDAAPARVGLGITTVLTMTTOSSGSRASL 	LSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRDEKDLGCCTKHYNTG :	VTTDNKLLRIFKNGNVLYSIRLTLILSCLMDLKNEPMDIQTCTMQLES	VTKTTMDYRVNVFLRQQWNDPRLSYRBYPDDSLDLDPSMLDS 	VALAKEEVKSGTKGSQPMSPSDFLDKLMGRTSGYDARTRPNFKGPPVNVTCNIFIN :	74.9%; Score 1687; DB 2; Similarity 92.3%; Pred. No. 3.7e-137; 4; Conservative 7; Mismatches 6;	> :X75850; NID:g435513; PIDN:CAA5 holine receptor mitter receptor; transmembrane	A499/0 liminary; nucleic acid sequence not shown pe: DNA .	B.; Maulet, Y.; Sefton, L.; Courtier, B. . 269, 2607-2612, 1994 ctural analysis of mouse glycine receptor umber: A49970; MUID:94132024; PMID:750792	tchain - mouse (fragment) (house mouse) quence_revision 17-Nov-1995 #	ALIGNMENTS	30.7 473 2 S53 30.6 473 2 S04 30.5 476 2 S31 30.5 476 2 S50 29.9 434 2 S50 29.7 449 2 A34 29.0 449 2 A34 29.0 449 2 T52 28.8 449 2 T52 28.7 465 2 A38 28.7 465 2 T37 28.2 474 2 S13 28.2 474 2 S13 28.3 474 2 S13
RLRRRORRORL 375	р — р 22 — 23	GCCTKHYNTGKFTCIEVKFH 264 	TCTMQLESSSILCSPLPSLS 204 TCTMQLE	DSIWKDDLFFANEKGANFHE 144 	NFKGPPVNVTCNIFINSFSS 84	Length 337; Indels 14; Gaps 1;	3468.1; PID:9817957 . protein		; Avner, P.; Guenet, J.L.; Betz alpha subunit genes. Identific 6	text_change 20-Aug-1999		gamma-aminobutyric gamma-aminobutyric gamma-aminobutyric gamma-aminobutyric gamma-aminobutyric avermectin-sensiti avermectin-sensiti gamma-aminobutyric gamma-aminobutyric gamma-aminobutyric hypothetical prote GABAA receptor del gamma-aminobutyric hypothetical prote gamma-aminobutyric gamma-aminobutyric gamma-aminobutyric gamma-aminobutyric gamma-aminobutyric

RESULT 2 \$12381 91ycine receptor alpha-2 chain - human

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C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_
C:Accession: S14816, S15776; JMO112
R:Akagi, H.; Hirai, K.; Hishinuma, F.
FEBS Lett. 281, 160-166, 1991
A:Title: Cloning of a glycine receptor subtype expressed A:Reference number: S14816; MUID:91200276; PMID:1707830
A:Accession: S14816
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 A;Status: not compared with A;Molecule type: mRNA A;Residues: 1-452 <KUH>A;Cross-references: GB:X6115
                                                                     A;Title: Alternative splicing A;Reference number: S15776; MI A;Accession: S15776
                                                                                                                      R; Kuhse, J.; Kuryatov, A.; Maulet, FEBS Lett. 283, 73-77, 1991
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A; Residues: 1-452 <GRE>
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                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-452 < AKA>
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                                                                                                                                     A;Cross-references: EMBL:X57281; NID:956743; PIDN:CAA40549.1; PID:956744 R;Kuhse, J.; Kuryatov, A.; Maulet, Y.; Malosio, M.L.; Schmieden, V.; Bet
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Date: 21-Nov-1993 #sequence
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   GB:X61159;
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MUID:91243883; I
 NID:g288344;
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Pred. No. 1.3e
29; Mismatches
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                                                                                     PMID:1645300
 PIDN: CAA43471.1;
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.3e-136;
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PID:g288345
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A; Residues: 1-193, 'E', 195-452 <nu².

A; Residues: 1-193, 'E', 195-452 <nu².

A; Residues: 1-193, 'E', 195-452 <nu².

C; Comment: Glycine reduces neuronal firing by activating this interpretation of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of 
A;Molecule type: mRNA
A;Residues: 1-452 <KUPA
C:Superfamily: acetylcholine receptor
C:Keywords: 9lycoprotein; membrane protein
F;1-27/Domain: signal sequence #status predicted
F;28-452/Product: 9lycine receptor alpha-2 chain
                                                                                                                                                                                                                                                                                                                                                                                           glycine receptor alpha-2 chain precursor variant B C; Species: Rattus norvegicus (Norway rat) C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 C;Accession: S18836
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A;Accession: JN0112
                                                                                                                                                                                                  A; Status: preliminary
                                                                                                                                                                                                                          A;Title: Alternative splicing A;Reference number: S15776; MC A;Accession: S18836
                                                                                                                                                                                                                                                                                                                                  R; Kuhse, J.; Kuryatov, FEBS Lett. 283, 73-77,
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A; Residues: 1-193, 'E', 195-452 < KU2>
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Neuron 5, 867-873, 1990
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A;Title: Structural analysis of mouse glycine receptor alpha subunit genes. A;Reference number: A49970; MUID:94132024; PMID:7507926
A;Accession: B49970
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A; Residues: 67-89 < KU
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                                                                                                                                                                               A;Gene: Glra2
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R;Kuhse, J.; Kuryatov, A.; Ma
                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-451 <MAT>
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                                                         Query Match
Best Local S
Matches 325
                                                                                                                                    ;Superfamily: acetylcholine receptor; transmembrane protein
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MTTLVPATLSFLLLWTLPGQVLLRVALAKE-EVKSGTKGSOPMSPSDFLDKLMGRTSGYD
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75.1%;
                                                         73.6%; Score 1656.5; DB 2; 75.1%; Pred. No. 2.2e-134; htive 33; Mismatches 48;
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Pred. No. 1
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1.3e-135; Indels
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A23682
glycine receptor alpha-3 chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change :
C;Accession: A23682
R;Kuhse, J; Schmieden, V; Betz, H.
J. Biol. Chem. 265, 22317-2230, 1990
A;Title: Identification and functional expression of a novel lig.
A;Reference number: A23682; MUID:91093073; PMID:2176214
A;Accession: A23682
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-464 <KUH>
A;Cross-references: GB:M55250; GB:M38385; NID:g204882; PIDN:AAA6
C;Superfamily: acetylcholine receptor
C;Keywords: transmembrane protein
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                                        KHYNTGKETCIEVKFHLERQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPARVGLGITT 308
                                                                                           QLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRDEKDLGCCT-
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                      KHYNTGKFTCIEVRFHLERQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPARVALGITT
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Pred. No. 8e-129;
                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NID: g204882; PIDN: AAA63492.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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R:Matzenbach, B.; Maulet, Y.; Sefton, L.; Courtier, B.; Avner, P.; Guenet, J.L.; Betz, I. Biol. Chem. 269, 2607-2612, 1994
A;Title: Structural analysis of mouse glycine receptor alpha subunit genes. Identificati A;Reference number: A49970; MUID:94132024; PMID:7507926
A;Accession: C49970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glycine receptor alpha-1 chain - mouse c;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 17-Mar-1999 C;Accession: C49970; S48662
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C49970
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C; Keywords: neurotransmitter receptor
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FEBS Lett. 350, 71-76, 1994
A;Title: Point mutation of 91ycine receptor alpha-1 subunit
A;Reference number: S48662; MUID:94341377; PMID:8062927
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A; Residues: 62-84 <SAU>
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A; Residues: 1-451 <MAT>
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                                                                                                                                                                                                                                                              MQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRDEKDLGCC
                                                                                                                                                                                                                                                                                                                                     WKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRLTLILSCLMDLKNFPMDIQTCT
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                                                       RRQRRQRLEEDIIQESRFYFRGYGLG-HCLQARDGGPMEGSGIYSP--QPPAPLLREGET
                                                                                                                                                                  TKHYNTGKFTCIEARFHLEROMGYYLIOMYIPSLLIVILSWISFWINMDAAPARVGLGIT
                                                                                                                                                                                                                                               MQLE-----
                                                                                                                                                                                                                                                                                                                  WKPDLFFANEKGAHFHEITTDNKLLRISRNGNVLYSIRITLTLACPMDLKNFPMDVQTCI
                                                                                                                                                                                                                                                                                                                                                                                           GPPVNVSCNIFINSFGSIAETTMDYRVNIFLRQQWNDPRLAYNEYPDDSLDLDPSMLDSI
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Pred. No. 1.9
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A; Residues: 1-449 <GRE>
A; Cross-references: GB: X52009; NID:g31850; PIDN:CAA36258.1; PID:g31851
C; Superfamily: acetylcholine receptor
C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R:Grenningloh, G.; Schmieden, V.; Schofield, P.R.; Seeburg, P.H.; Siddique, T.; Mol
EMBO J. 9, 771-776, 1990
A:Title: Alpha subunit variants of the human glycine receptor: primary structures,
A; Reference number: S12381; MUID:90183975; PMID:2155780
A; Accession: S12382
                                                                                                                                                                                                   glycine receptor alpha-1 chain - rat
C;SpecLes: Rattus norvegicus (Norway rat)
C;Date: 20-reb-1995 #sequence_revision 20-Feb-1995
C;Accession: S20662; A38597; A27141
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A;Cross-references: EMBL;X55246; NID:g56468; PIDN:CAA38987.1; PID:g56469 R;Malosio, M.L.; Grenningloh, G.; Kuhse, J.; Schmieden, V.; Schmitt, B.; J. Biol. Chem. 266, 2048-2053, 1991
                                                 A; Molecule type: mRNA
A; Residues: 1-457 < MAL>
                                                                                        A; Status: preliminary
                                                                                                           A; Reference number: A; Accession: $20662
                                                                                                                                           R;Malosio, M.; Kuhse, J.; Betz, H. submitted to the EMBL Data Library, December 1990 A;Description: Complete coding sequence of the an
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307; Conser
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Pred. No. 7.5e
38; Mismatches
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P.;

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glycine receptor beta chain - mouse ()Species: Mus musculus (house mouse) ()Species: Mus musculus (house mouse) ()C;Date: 20:Feb-1995 #sequence_revision 20:Feb-1995 #text_change 20:Aug-1999 ()Accession: S46499; 148371; I48372 R;Kingsmore, S.F.; Giros, B.; Suh, D.; Bieniarz, M.; Caron, M.G.; Seldin, M. Nature Genet. 7, 136-141, 1994 A;Title: Glycine receptor beta-subunit gene mutation in spastic mouse associ A;Reference number: S46459; MUID:95004576; PMID:7920630 A;Accession: S46459.
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A;Title: The strychnine-binding subunit of A;Reference number: A27141; MUID:87258250; A;Accession: A27141
A;Molecule type: mRNA
A;Moslecule type: mRNA
A;Residues: 23-353,362-457 <GRE>
C;Superfamily; acetylcholine receptor
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C;Keywords: alternative splicing
A;Molecule type: mRNA
A;Residues: 1-496 <KIN>
A;Residues: 1-496 <KIN>
A;Cross-references: EMBL:U09399; NID:g508234; PIDN:AAA61874.1; PID:g508235
R;Cross-references: EMBL:U09399; NID:g508234; PIDN:AAA61874.1; PID:g508235
R;Cross-reference, M.; Gass, P.; Simon-Chazottes, D.; Guenet, J.L.; F
R;Mulhardt, C.; Fischer, M.; Gass, P.; Simon-Chazottes, D.; Guenet, J.L.; F
Neuron 13, 1003-1015, 1994
A;Title: The spastic mouse: aberrant splicing of glycine receptor beta subla R;Reference number: I48371; MUID:95033198; PMID:7946325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Alternative splicing generates two variants of A;Reference number: A38597; MUID:91115810; PMID:1703526 A;Accession: A38597
A;Status: preliminary
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A; Residues: 316-378 <MA2>
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71.5%;
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Pred. No. 8.2
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3.2e-127;
hes 57;
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Zensen, M.;
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                         beta subunit mRNA
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A;Molecule type: protein
A;Rosidues: 103-108;124-136;213-234 <GR2>
A;Experimental source: spinal cord, brain
C;Comment: The glycine receptor is a ligand-gated chloride channel in postsynaptic me
C;Comment: The glycine receptor contains two membrane-spanning subunits of 48kd, alph
C;Superfamily: acetylcholine receptor
C;Keywords: glycoprotein; phosphoprotein; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-496/Product: glycine receptor beta chain #status predicted <GRB>
F;270-286/Domain: transmembrane #status predicted <TM1>
F;289-316/Domain: transmembrane #status predicted <TM2>
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A; Residues: 100-250 < RE2>
- ^-^- references: EMBL: X81201; NID: 9557656;
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JH0165
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A;Accession: I48372
                                                                                                                                                                                                                                                                                                                                                                                R;Grenningloh, G.; Pribilla,
Neuron 4, 963-970, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                        N;Alternate names: glycine receptor 58K chain precursor C;Species: Rattus norvegicus (Norway rat) C;Date: 31-Dec-191 #sequence_revision 31-Dec-1991 #text_change C;Accession: JH0165; PS0296
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A; Introns: 176/2; 204/1
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A; Residues: 13-364, 'A', 366-496 < RES>
                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-496 <GRE>
A; Accession: PS0296
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A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                     A; Reference number: JH0165; A; Accession: JH0165
                                                                                                                                                                                                                                                                                                                                       A; Title: Cloning and expression of the 58 kd beta subunit of the inhibitory glycine A; Reference number: JH0165; MUID:90297968; PMID:2163264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLFVF 344
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C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change
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F;478-495/Domain: transmembrane #status predicted <TM4>
F;478-495/Domain: transmembrane #status predicted <TM4>
F;54,242,387/Binding site: carbohydrate (Asn) (covalent) #status predicted F;183-197,243-255/Disulfide bonds: #status predicted F;385,410/Binding site: phosphate (Thr) (covalent) #status predicted F;435/Binding site: phosphate (Tyr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                   A; Cross-references: GDB:5875373; OMIM:138492
A; Map position: 4q32-4q32
                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, A; Reference number: G09080 A; Accession: G02031
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R;Handford, C.A.; S
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A; Residues: 1-497 <HAN>
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                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                            ;Gene: GDB:GLRB
                                                                                                                                                                                                                                                                                  Superfamily: acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                  Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary; translated
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      --SYREYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIR
                                             RLL---VSYDPRIRPNFKGIPVDVVVNIFINSFGSIQETTMDYRVNIFLRQKWNDPRLKL
                                                                                 KLMGRTSGYDARIRPNFKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRL--
                                                                                                                      TTAFLILISL----WVEEAYSKEKSSKKGKGKKKQYLCPSQQSAEDLARVPANSTSNILN
                                                                                                                                                             TLSFLLLWTLPGQVLLRVALAKEEVKSGTKGSQPM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASLVEYAVVQVMLNNPKRVEAEKARIAKAEQ 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AALLEYAAI ----NFVSRQHKEFIRLRRRQR 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLFVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L-EKIALPQFDIKKEDIEYGNCTKYYKGTGYYTCVEVIFTLRRQVGFYMMGVYAPTLLIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VAEGLTLPQF-ILRDEKDLGCCTKHY-NTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SITLSCPLDLTLFPMDTQRCKMQLE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSFFILMSL----LFEDACSKEKSSKKGKGKKKQYLCPSQQSAEDLARVPPNSTSNILNR
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                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schofield, P.R.
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47.8%; Pred. No. 3.
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                                                                                                                                                                                                                       Score 855.5;
Pred. No. 1.7
                                                                                                                                                                                                                                                                                                                                                                              NID:g992686; PIDN:AAB37750.1;
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3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   August
                                                                                                                                                                                                  Mismatches
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ches 88;
                                                                                                                                                                                                                 .7e-65;
                                                                                                                                                                                                                                         DB 2;
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                                                                                                                                                                                                    99;
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                                                                                                                                                                                                                                         Length
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                                                                                                                                                             -SPSDFLD
                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Keywords: glycoprotein; neurotransmitter receptor; transmembrane protein F;1-23/Domain: signal sequence #status predicted <SIG> F;24-499/Product: gamma-aminobutyric acid/benzodiazepine receptor A beta chain #statu F;24-499/Product: gamma-aminobutyric acid/benzodiazepine receptor A beta chain #statu F;32,98,106,152,334,367,489/Binding site: carbohydrate (Asn) (covalent) #status predi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Cloning of genomic A;Reference number: A60170; A;Recession: A60170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:X58638; NID:99626
A;Note: the translated sequence in GenBank entry LSGABAA,
R;Harvey, R.J.; Vreugdenhil, E.; Barnard, E.A.; Darlison,
Biochem. Soc. Trans. 18, 438-439, 1990
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A; Residues: 201-231, 'L', 233-334 <HAR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: nucleic acid sequence not shown;
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A;Title: Sequence of a functional invertebrate GABA(A) receptor subunit A;Raference number: S17785; MUID:92007774; PMID:1655414
A;Accession: S17785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Lymnaea stagnalis (great pond snail)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 20-Aug-1999
C;Accession: S17785; A60170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gamma-aminobutyric acid/benzodiazepine receptor A beta chain precursor - N; Alternate names: GABA(A) receptor
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                                                             198
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                                                                                                                                                                                                                                                                                                                           48 LDKLMGRTSGYDARIRÞNFKGPÞVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDÞRL
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YIPSLLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWM
                                                                                                                                                                                                                                                            SYREYPDDSLDLDP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVAEGLTLPQF-ILRDEKDLGCCTKHY-NTGKFTCIEVKFHLEROMGYYLIQMYIPSLLI 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YWLNDRGAVTGVEDVSLPQFSITNYATIN-KIEELSTGDYQRLSLIFQLQRNIGYFIFQT
                                                                                                                                                                                                                     QF--IFNESLDLGENRSVTTMTLTGAFAEKIWVPDTFLANDKNSFLHDITEKNKMVRLYG
                                                                                                                                                                                                                                                                                                IDSLL---KGYDIRLRPSFGGAPLEIGIEVILASFDSISEVDMDYTITMYLNQYWRDERL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FAALLEYAAI - - - - NEVSRQHKEFIRLRRRQR 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAV 225
                                                                                                  EWLEDAPAVQVAEGLTLPQFILRDEKDLGCCTKHYNTGKFTCIEVKFHLERQMGYYLIQM
                                                                                                                                           NGSLVYGMRFTTTLACMMDLHNYPLDHQECTVEIE
                                                                                                                                                                            NGNVLYSIRLTLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVF 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVLSWLSFWINPDASAARVPLGIFSVLSLASECTTLAAELPKVSYVKALDVWLIACLLFG
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                                                                                                                                                                                                                                                                                                                                                                                               32.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and cDNA sequences encoding an invertebrate MUID:90323312; PMID:2164988
                                                                                                                                                                                                                                                                                                                                                                            74;
                                                                                                                                                                                                                                                                                                                                                                        Score 742; DB 2; Pred. No. 9.6e-56; "" matches 90;
                                                                                                                                                                                                                                                          SMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFK 156
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                                                                                                                                                                                                                                                                                                                                                                                                               Length 499;
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gamma-aminobu

(PID:g9627)

36;

Gaps

93 107

336 256 276 197 subunit which can

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280

221

translation

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A; Molecule type: mRNA
A; Residues: 357-360, 357-366 <LA2>
R; Bateson, A.N.; Lasham, A.; Darlison, M.G.
submitted to the EMBL Data Library, November 1990
A; Description: Gamma-aminobutyric acid-A receptor heterogeneity is increased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gamma-aminobutyric acid receptor A beta-4' chain precursor - N; Contains: gamma-aminobutyric acid receptor A beta-4 chain, C; Species: Gallus gallus (chicken)
                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 28-360,365-405 <BA4>
A;Residues: 28-360,365-405 <BB4>
C;Comment: The gamma-aminobutyric acid A receptor is the major inhibitory neurotransmiti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Lasham, A.; Bateson, A.N.; Darlison, M.G.
BioChem. Soc. Trans. 19, 95, 1991
A;Tille: Alternative splicing increases GABA-A receptor heterogeneity.
A;Reference number: A61282; MUID:91244095; PMID:1645322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Gamma-aminobutyric acid A receptor heterogeneity is increased by alternative A;Reference number: JH0359; MUID:91162222; PMID:1848280 A;Accession: JH0359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 20-Aug-1999 C;Accession: JH0359; JH0360; B61282; A61282; S29694; S29696; S29695 R;Bateson, A.N.; Lasham, A.; Darlison, M.G. J. Neurochem. 56, 1437-1440, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X56647; NID:g62916; A;Accession: S29695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-405 <BA3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: EMBL: X56646; NID: g62912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: S29694
A; Accession: S29694
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A; Residues: 357-366 <LAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X56
A;Experimental source: brain
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A; Residues: 1-488 <BAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession:
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A; Residues: 364-488 <BAW>
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A;Experimental source: brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: B61282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type:
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                                                                                                                                                                                                                                                                                                                          ;Superfamily: acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lasham, A.; Bateson, A.N.;
                                                                                                      448/Binding site:
                                             Local Similarity
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                           Conservative
                                                                                                      phosphate (Ser)
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                                         32.2%;
                           79;
                                       Score 726;
Pred. No. 2.
                                                                                                    (covalent) #status predicted
                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               PIDN:CAA39969.1;
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                                       DB 2;
1.2e-54;
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                                                            Length 488;
                      Indels
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                      52;
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A;Residues: 1-533 <THO>
A;Cross-references: GB:U28803; NID:9881589; PIDN:AAA68961.1; PID:9881590
C;Superfamily: acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cyclodiene insecticide resistance protein - yellow fever mosquito
C;Species: Aedes aegypti (yellow fever mosquito)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Thompson, M.; Shotkoski, F.; FEBS Lett. 325, 187-190, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: S33744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            331 AIDIWMAVCLLFVFAALLEYAAINFVSRQ----HKEFIRLRR--RQRRQRLEE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                368 GNILLSTLDMNNELLATDMMSSVGDSRNSVMSFEGSGIQFRKPLAS--RDG 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  275 QMYIPSLLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDI 334
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                                                                                                  YYLIOMYIPSLLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVK 330
                                                                                                                                                                                 MKDLVFEWLEDAPAVQVAEGLTLPQFILRDEKDLGCCTKHYNTGKFTCIEVKFHLERQMG
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                                                            YYLIQIYIPSGLIVIISWVSFWLNRDATPARVALGVTTVLTMTTLMSSTNAALPKISYVK
                                                                                                                                         MRDIRYFWKDGLSSVGMSSEVELPQFRVLGHRQ-RATEINLTTGNYSRLACEIQFVRSMG
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Pred. No. 3.7e-54;
0; Mismatches 122;
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Search co Job time	Db	Qy	Db
)mple : 29	384	378	324
Search completed: June 25, 2003, 17:17:34 Job time : 29.9262 secs	384 PPVSDHSHGHGHSHGH 401	378 -DIIQESRFYFRGYGLGH 394	324 SIDVYLGTCFVMVFASLLEYATVGYMAKRIQIGKQRFMAIQKIAEQKKQQAADANHPPPP 383

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OM protein - protein search, using sw model

Run on: June 25, 2003, 17:12:59; Search time 17.3557 Seconds (without alignments) 1029.995 Million cell updates/sec

Title: Perfect score: Sequence:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

US-10-075-846-4
2252
1 MTTLVPATLSFLLLWTLPGQ......PQPPAPLLREGETTRKLYVD 431

Searched: 112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

30 32 33	17 18 19 20 21 22 22 23 24 28 29	3 5 5 5 6 6 7 7 6 8 8 11 11 11 11 11 11 11 11 11 11 11 11	Result No.
653.5 652.5 644.5	715 712 712 712 696 697 694.5 694.5 691.5 687.5 664.5	1678 1672.5 1592.5 1580.5 1580.5 1589.5 1569.5 1569.5 1569.5 1769.5 1769.5 1769.5 1769.5 1769.5	score
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GAAP RAT GAAP RAT GAAD MOUSE GAAP HUMAN GAR2_HUMAN	GAB3_DROME GAB2_HUMAN GAB2_HOUSE GAB1_MOUSE GAB3_HUMAN GAB1_ROT GAB1_BOVIN GAB1_BOVIN GAB3_HOUSE GAB1_HUMAN GAB3_CHICK GAD_HUMAN GAB3_CHICK GAD_RAT	01 5 2 2 3 3 1 1 1 1 1 1 1 1 1	ID GRA2_HUMAN
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27.9	. 28.0	28.0	28.0	28.1	28.2	28.2	28.2	28.3	28.4	28.4	28.4
467	552	552	473	465	474	453	474	632	453	474	453
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GAC3_MOUSE	GAA4_RAT	GAA4_MOUSE	GAR1_HUMAN	GAA6_CHICK	GAC2_CHICK	GAA6_RAT	GAR1_RAT ·	GAAT_HUMAN	GAA6_MOUSE	GAR1_MOUSE	GAA6_HUMAN
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P27681	P28471	Q9d6f4	P24046	Q90845	P21548	P30191	P50572	Q9un88	P16305	P56475	Q16445
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-!- SUBCELLULAR LOCATION: Integral membrane protein!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA-** (SHOWN HERE) AND ALPHA- 2B; ARE PRODUCED BY ALTERNATIVE SPLICING!- MISCELLANEOUS: THE ALPHA SUBUNIT BINDS STRYCHNINE!- SIMILARITY: BELONGS TO THE LICAND-CATED IONIC CHANNEL FAMILY	SEQUENCE OF 1-360 FROM N.A. MEDLING-97129407; PubMed-8973915; MODANI U.R., Burghes A.H.M.; MODANI U.R., Burghes A.H.M.; "Structure of the human alpha 2 subunit gene of the glycine receptor: use of vectorette and Alu-exon PCR."; Genome Res. 6:1200-1206(1996). -i- FUNCTION: THE GLYCINE RECEPTOR IS A NEUROTRANSMITTER-GATED ION CHANNEL. BINDING OF GLYCINE TO ITS RECEPTOR INCREASES THE CHLORIDE CONDUCTANCE AND THUS PRODUCES HYPERPOLARIZATION (INHIBITION OF NEURONAL FIRING). -i- SUBUNIT: PENTAMER COMPOSED OF ALPHA (48 kDa) AND BETA (58 kDa) SUBUNITS. A THIRD TYPE OF SUBUNIT (93 kDa) IS A PERIPHERAL MEMBRANE PROTEIN ASSOCIATED WITH THE CYTOPLASMIC DOMAINS OF THE RECEPTOR CORE.	SEQUENCE FROM N.A. MEDLINE-90183975; PubMed-2155780; Grenningloh G. Schmieden V., Schofield P.R., Seeburg P.H., Grenningloh G. Schmieden V., Becker C.M., Betz H.; **Riddique T., Mohandas T.K., Becker C.M., Betz H.; **PAlpha subunit variants of the human glycine receptor: primary **PALPha subunit variants of the human glycine receptor of the **Corresponding genes."; EMBO J. 9:771-776(1990). **EMBO J. 9:771-776(1990). **EQUENCE FROM N.A. **MEDLINE-9837669; PubMed-9674912; Cummings C.J., Dahle E.J.R., Zoghbi H.Y.; **PANALYSIS of the genomic structure of the human glycine receptor **Analysis of the genomic structure of the human glycine receptor **alpha-2 subunit gene and exclusion of this gene as a candidate for **Rett syndromee."; **Am. J. Med. Genet. 78:176-178(1998). **Am. J. Med. Genet. 78:176-178(1998).	_HUMAN _HUMAN STANDARD; PRT; 452 AA. P23416; 099862; 01-NOV-1991 (Rel. 20, Created) 01-NOV-1991 (Rel. 20, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update) Glycine receptor alpha-2 chain precursor. GLAR2. HOmo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;

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Pfam; PF02932; Neur_Chan_memb; 1.
TIGRPAMS; TIGR00860; LIC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94132024; PubMed=7507926;
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ities requires a license
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MISCELLANEOUS: THE ALPHA SUBUNIT BINDS STRYCHNINE.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL
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SUBUNIT: PENTAMER COMPOSED OF ALPHA (48 kDa) ISSUBUNITS. A THIRD TYPE OF SUBUNIT (93 kDa) ISMEMBRANE PROTEIN ASSOCIATED WITH THE CYTOPLAS
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channel;
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a novel variar
                                                                                          Glycoprotein;
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novel variant.";
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MBL outstation -
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P22771; Q91W28;
01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Glycine receptor alpha-2* chain precursor (Neonatal isoform)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
NON_TER
                                                                                                                                                               Kuhse J., Schmieden V., Betz H
"A single amino acid exchange
glycine receptor subunit.";
Neuron 5:867-873(1990).
                                                                                           SEQUENCE FROM N.A.
STRAIN-Wilstar; TISSUE-Spinal cord;
MEDLINE-91200276; PubMed-1707830;
Akagi H., Hirai K., Hishinuma F.;
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
  MEDLINE-91243883;
               SEQUENCE FROM N.A.
TISSUE-Brain;
                                                   "Cloning of a glycine receptor subtype expressed spinal cord during a specific period of neuronal FEBS Lett. 281:160-166(1991).
                                                                                                                                                                                                                  MEDLINE-91097798;
                                                                                                                                                                                                                                                                        NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                           (Glycine receptor strychnine binding subunit).
                                                                                                                                                                                                                                             EQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Loca 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VTETTMDYRVNVFLRQQWNDPRLAYREYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VALAKEDVKSGLKGSQPMSPSDFLDKLMGRTSGYDARIRPNFKGPPVNVTCNIFINSFGS
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  PubMed-1645300;
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255
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162
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337
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                                                                                                                                                                                                                                                                                      Rodentia;
                                                                                                                                                                                                                                                                                                   Chordata;
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92.08;
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EXTRACELLULAR (PROBABLE).
POTENTIAL.
POTENTIAL.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1678; DB 1;
Pred. No. 1.3e-135;
Pred. No. 1.3e-135;
                                                                                                                                                                                          alters
                                                                                                                                                                                                                                                                                     Craniata; Vertebrata;
Sciurognathi; Muridae
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                                                                                                                                                                                                                                              OF,
                                                                                                                                                                                          the
                                                                                                                                                                                                                                              GLU-194
                                                                                                                                                                                        pharmacology of neonatal
                                                                                                                                                                                                                                                                                      Muridae;
                                                                  in rat brain and development.";
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Murinae; Rat
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 CARBOHYD
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DISULFID
CARBOHYD
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SITE
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TRANSMEM
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                                                                                                                                                                            CHAIN
                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                            TIGRFAMs;
                                                                                                                                                                                                                                                          PRINTS; PR00252;
                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                         DOMAIN
                                                                                                                        TRANSMEM
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284
254
287
319
343
194
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243
72
103
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452
253
280
304
342
423
423
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-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCED SY ALTERNATIVE SPLICING.
-!- ALTERNATIVE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: THE GLYCINE RECEPTOR IS ABUNDANT IN THE SPINAL CORD AND BRAINSTEM OF VERTEBRATES.
-!- DEVELOPMENTAL STAGE: THE ALPHA-2* SUBUNIT ISOFORM IS PRESENT ONLY IN NEONATAL RATS. ISOFORMS ALPHA-2A AND ALPHA-2B ARE PRESENT IN THE PRE- AND NEONATAL BRAIN. AT LATER POSTNATAL STAGES, ALPHA-2A LEVELS GREATLY DECREASE WHILE ALPHA-2B IS BARELY DETECTABLE.
-!- MISCELLANEOUS: THE ALPHA SUBUNIT BINDS STRYCHNINE.
-!- MISCELLANEOUS: THE ALPHA SUBUNIT BINDS STRYCHNINE.
-!- MISCELLANEOUS: IDENTICAL TO THE HUMAN ALPHA-2 SUBUNIT, EXCEPT FOR SUBSTITUTIONS AT POSITION 194 (G -> E). ACCOUNTS FOR THE LOWER STRYCHNINE SENSITIVITY OBSERVED IN NEONATAL RATS.
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Alternative splicing generates two of the inhibitory glycine receptor FEBS Lett. 283:73-77(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              recombinant alpha 1 glycine receptors.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-i-FUNCTION: THE GLYCINE RECEPTOR IS A NEUROTRANSMITTER-GATED ION
CHANNEL. BINDING OF GLYCINE TO ITS RECEPTOR INCREASES THE CHLOR
CONDUCTANCE AND THUS PRODUCES HYPERPOLARIZATION (INHIBITION OF
                                                                                                                   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein;
                                                                                                                                                                                                                                                InterPro; IPR000188; GABAA_recepto InterPro; IPR001175; Neur_channel. Pfam; PF02931; Neur_chan_LBD; 1. Pfam; PF02932; Neur_chan_memb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beato M., Groot Kormelink P.J., Colquhoun D., Sivilo "Concentration dependence of single channel currents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kuhse J., Kuryatov A., Betz H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Sprague-Dawley; TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEURONAL FIRING).
SUBUNIT: PENTAMER COMPOSED OF ALPHA (48 kDa) AND BETA (58 KE SUBUNITS. A THIRD TYPE OF SUBUNIT (93 kDa) IS A PERIPHERAL MEMBRANE PROTEIN ASSOCIATED WITH THE CYTOPLASMIC DOMAINS OF RECEPTOR CORE.
                                                                                                                                                                                                                                                                                                                                                                              JN0112; JN0112.
S14816; S14816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X57281; CAA40549.1; -. X61159; CAA43471.1; -.
                                                                                                                                                                                        TIGR00860;
                                                                                               Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                CAC35981.1;
                                                                                                                                                                                                                      NRIONCHANNEL.
                                                                                                                                                                                     LIC; 1
                                                                                                                                                                                                                                                                                                                                                   GABAA_receptor.
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                                                                                               family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   is not removed. Usage by and the state of announce/
agreement (See http://www.isb-sib.ch/announce/
EXTRACELLULAR
                             GLYCINE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         two isoforms
                                                                                            Alternative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           kDa) AND BETA (58 kDa)
Da) IS A PERIPHERAL
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                                                                                            splicing
                                 ALPHA-2* CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the
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tent is in
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BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAN-LINKED) (GLCNAN-LINKED)

(GLCNAC. . .) (POTENTIAL)
(GLCNAC. . .) (POTENTIAL)

BINDING PROBABLE CYTOPLASMIC PROBABLE PROBABLE. PROBABLE

IMPORTANT

FOR

GLYCINE

AND

STRYCHNINE

(PROBABLE)

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Best Local
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                                                                                                                                                                                                                                                    GRAJ_HUMAN.
O75311; O75816;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
15-Jun-2002 (Rel. 41, Last annotation updat)
                                                     TISSUE-Fetal brain;
MEDLINE-98344067; PubMed-9677400;
Nikolic Z., Laube B., Weber R.G., Lichter P., Kioschis P., Poustka Muelhardt C., Becker C.-M.;
"The human glycine receptor subunit alpha3. GLRA3 gene structure, chromosomal localization, and functional characterization of alternative transcripts.";
J. Biol. Chem. 273:19708-19714(1998)
J. Biol. Chem. 273:19708-19714(1998)
-i- FUNCTION: THE GLYCINE RECEPTOR IS A NEUROTRANSMITTER-GATED ION CHANNEL. BINDING OF GLYCINE TO ITS RECEPTOR INCREASES THE CHLOS CONDUCTANCE AND THUS PRODUCES HYPERPOLARIZATION (INHIBITION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
MUTAGEN
                                                                                                                                                                                                                                                                                                                                               MAMDH.
                                                                                                                                                                                                             Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                           Eukaryota;
Mammalia;
                                                                                                                                                                                        SEQUENCE FROM N.A.
NEURONAL FIRING).

SUBUNIT: PENTAMER COMPOSED OF LIGAND BINDING ALPHA (48 kDa) STRUCTURAL BETA (58 kDa) SUBUNITS. A THIRD TYPE OF SUBUNIT (kDa) IS A PERIFHERAL MEMBRANE PROTEIN ASSOCIATED WITH THE CYTOPLASMIC DOMAINS OF THE RECEPTOR CORE.
                                                                                                                                                                                                             sapiens (Human).
ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                         345
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75.38;
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E->G: INCRE
STRYCHNINE.
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Pred. No. 9
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.3e-135;
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                                                                     CHLORIDE
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Best Local S
Matches 312
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                                                                                                                                                                                                                                                                                 DISULFID DISULFID
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000188; GABAA_receptor.
InterPro; IPR001175; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF017724; AAC39919.1; EMBL; AF017715; AAC39919.1; EMBL; AF017716; AAC39919.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA3L (SHOWN HERE)
ALPHA3K; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: WIDELY DISTRIBUTED THROUGHOUT THE
                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
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DOMAIN: THE N-TERMINAL DOMAIN CARRIES STRUCTURAL DETERMINANTS ESSENTIAL FOR AGONIST AND ANTAGONIST BINDING. TM2 IS THOUGHT T FORM THE INNERT WALL OF THE CHLORIDE CHANNEL THE CYTOPLASMIC FORM THE INNERT WALL OF THE CHLORIDE CHANNEL INACTIVATION KINETICS. AN IMPORTANT DETERMINANT OF CHANNEL INACTIVATION KINETICS. MISCELLANEOUS: THE ALPHA SUBUNIT BINDS STRYCHNINE.

MISCELLANEOUS: THE ALPHA SUBUNIT BINDS STRYCHNINE.

SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration -
sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                  Similarity
             FHEVTTDNKLLRIFKNGNVLYSIRLTLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS00236; NEUROTR_ION_CHANNEL;
                                                                     FSSVTKTTMDYRVNVFLRQQWNDPRLSYREYPDDSLDLDPSMLDSIWKPDLFFANEKGAN
                                                                                                                             LLRVALAKEEVKSGTKGSQPMSPSDFLDKLMGRTSGYDARIRPNFKGPPVNVTCNIFINS
FHEVTTONKLLRIFKNGNVLYSIRLTLTLSCPMDLKNFPMDVQTCIMQLE---
                                                      FGSTAETTMDYRVNTFLRQKWNDPRLAYSEYPDDSLDLDPSMLDSTWKPDLFFANEKGAN
                                                                                                              LLLSLVATKETDSARSRSAPMSPSDFLDKLMGRTSGYDARIRPNFKGPPVNVTCNIFINS
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BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
MISSING (IN ISOFORM ALPHA3K).
MISSING (IN REF. 1; AAC39917).
; B8A267A31C0C6E64 CRC64;
                                                                                                                                                                                  Score 1602.5; DB 1; Pred. No. 5.5e-129;
                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                 GLYCINE RECEPTOR
                                                                                                                                                                                                                                                                                                               PROBABLE
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PIR; A23682; A23682.

InterPro; IPR000188; GABAA_receptor.
InterPro; IPR001175; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
TIGRFAMS; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic chansmembrane; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                    between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRA3_RAT
P24524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sent
15-JUN-2002 (Rel. 41, Last anno
Glycine receptor alpha-3 chain
                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kuhse J., Schmieden V., Betz H.;
"Identification and functional expression of a subunit of the inhibitory glycine receptor.",
J. Biol. Chem. 265:22317-22320(1990).
                                                                                                                                                                                                            EMBL; M55250;
PIR; A23682; /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91093073; PubMed=2176214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLRA3
                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Integral membrane protein.
MISCELLANEOUS: THE ALPHA SUBUNIT BINDS STRYCHNINE.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONDUCTANCE AND THUS PRODUCES HYPERPOLARIZATION (INHIBITION OF MEURONAL FIRING).

SUBUNIT: PENTAMER COMPOSED OF ALPHA (48 kDa) AND BETA (58 kDa) SUBUNITS. A THIRD TYPE OF SUBUNIT (93 kDa) IS A PERIPHERAL MEMBRANE PROTEIN ASSOCIATED WITH THE CYTOPLASMIC DOMAINS OF TH
                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Eleuropean Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1101. Chem. 265:22317-22320(1990).
FUNCTION: THE GLYCINE RECEPTOR IS A NEUROTRANSMITTER-GATED CHANNEL. BINDING OF GLYCINE TO ITS RECEPTOR INCREASES THE CHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RECEPTOR CORE
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Rodentia;
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; Murinae; Rat
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CHAIN
DOMAIN
TRANSMEM
TRANSMEM
SEQUENCE FROM N.A.

MEDLINE-90183975; PubMed-2155780;

Grenningloh G., Schmieden V., Schofield P.R., Seeburg P.H.,

Siddique T., Mohandas T.K., Becker C.-M., Betz H.;

*Alpha subunit variants of the human glycine receptor: primary

*structures, functional expression and chromosomal localization

corresponding genes.*;

EMBO J. 9:771-776(1990).
                                                                                                                                                                                                                                                                                                           01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
01-VUN-2002 (Rel. 41, Last annotation updat
01-VUN-2002 (Rel. 41, Last annotation updat
01-VUN-2002 (Rel. 41, Last annotation updat
01-VUN-2002 (Rel. 20, Last sequence update)
01-VUN-2002 (Rel. 20, Last sequence update)
01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
01-NOV-1991 
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P23415;
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SEQUENCE
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                              Homo
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Primates;
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CYTOPLASMIC
PROBABLE.
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Pred. No. 4.3e-128;
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BY SIMILARITY.
N-LINKED (GLCNAC. . .) (P
. 5A429F4C6F16E40D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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VARIANTS
                                                                                                                                                                       MEDLINE=97220600; PubMed=9067762;
Seri M., Bolino A., Galietta L.J.V., Lero
"Startle disease in an Italian family by
subunit of the inhibiting glycine recepto
Hum. Mutat. 9:185-187(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                         mutation in a family paraparesis.";
J. Med. Genet. 33:43:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96311686; PubMed=8733061;
Elmsile F.V., Hutchings S.M., Spe
Gardiner R.M., Rees M.;
"Analysis of GLRA1 in hereditary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT STHE CYS-307.

MEDLINE=95336157; PubMed=7611730;

Shiang R., Ryan S.G., Zhu Y.-Z., Fielder T.J.,

Yamashita S., O'Connell P., Wasmuth J.J.;

"Mutational analysis of familial and sporadic
Ann. Neurol. 38:85-91(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Evidence for recessive as well as unique the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of th
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the alpha 1 subunit of the inhibitory
Hum. Mol. Genet. 3:1201-1201(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shiang R., Ryan S.G., Zhu Y.-Z., O'Connell P., We "Mutational and haplotype analysis of the aplhal glycine receptor in hyperekplexia patients."; Am. J. Hum. Genet. 55:A242-A242(1994).
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MEDLINE-94129612; PubMed-8298642;
Shiang R., Ryan S.G., Zhu Y.-Z., Hahn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-96152139; PubMed-8571969; Milani N., Dalpra L., del Prete A., "A novel mutation (266 Gln-->His) i
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VARIANTS STHE HIS-280 AND HIS-420.
MEDLINE-99442259; PubMed-10514101;
Vergouwe M.N., Tilssen M.A., Peter
"Hyperekplexia phenotype due to co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inhibitory glycine-receptor gene (GLRA1)
hyperekplexia.";
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MEDLINE-96152139; Pub
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MEDLINE-95187157; PubMed-7881416;
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;; PubMed=7981700;

regia G., Bernasconi A., Re

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as well as dominant forms of startle disease
as well as in the alpha 1 subunit of the
Peters A.C.,
to compound
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in the alpha 1 subunit of the
(GLRA1) in hereditary
                                                                                                                                                                                                              receptor.";
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for hyperekplexia and spa:
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glycine receptor
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   heterozygosity
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Frants R.R.
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                                                                                                                                                                                                                                              , Romeo G.;
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                                                                                                                                                                                                                                                                                                                                 Pfam; PF02931; Neur_chan_LBD; 1. Pfam; PF02932; Neur_chan_memb; 1.
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"Novel GLRA1 missense mutation (P250T)
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DISEASE: DEFECTS IN GLRAI ARE A CAUSE OF HYPEREKPLEXIA (OR
DISEASE: STHE); AN AUTOSOMAL DOMINAMT NEUROLOGIC DISORDER
CHARACTERIZED BY MUSCULAR RIGIDITY OF CENTRAL NERVOUS SYSTE
ORIGIN, PARTICULARLY IN THE NEONATAL PERIOD, AND BY AN EXAG
STARTLE RESPONSE TO UNEXPECTED MOCOUSTIC OR TACTILE STIMULI.
MISCELLANEOUS: THE ALPHA SUBUNIT BINDS STRYCHNIME.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEURONAL FIRING).
SUBUNIT: PENTAMER COMPOSED OF ALPHA (48 kDs SUBUNITS, A THIRD TYPE OF SUBUNIT (93 kDa) MEMBRANE PROTEIN ASSOCIATED WITH THE CYTOPI
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HGNC:4326; GI
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IPR001175; Neur_channel.
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SIMILARITY).
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             POTENCY
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                                                                                                                                                                                                                                                                                     Signal;
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GRALDOVIN
ID GRALB
AC P57695
DT 16-CCT
DT 16-CT
DT 15-JUN
DE GLUCIN
GN GLRA1.
OC EUROY
OC EUROY
OC EUROY
OC HAMMAL
OC EUROY
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OC HOVIDA
ON HEALY
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                                                                                                                                                                                                                                                                                                                                                                                                        GRA1_BOVIN
P57695;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Glycine receptor alpha-1 chain precursor (Glycine subunit) (Strychnine binding subunit)
              "A nonsense mutation in the alphal subunit of the inhibitory gly receptor associated with bovine myocionus.";

Mol. Cell. Neurosci. 17:354-363(2001)
-I- FUNCTION: THE GLYCINE RECEPTOR IS A NEUROTRANSMITTER-GATED I CHANNEL. BINDING OF GLYCINE TO ITS RECEPTOR INCREASES THE CH CONDUCTANCE AND THUS PRODUCES HYPERPOLARIZATION (INHIBITION NEURONAL FIRING) (BY SIMILARITY).
                                                                                                                                        Pierce K.D., Handford C.A., Morris Healy P.J., Schofield P.R.;
                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-21109390;
                                                                                                                                                                                                                NCBI_TaxID=9913;
                                                                                                                                                                                                                                                 Bovidae;
                                                                                                                                                                                                                                                             Mammalia; Eutheria;
                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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   NEURONAL
SUBUNIT:
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R -> Q (IN STHE; DEC!
GLYCINE TO ACTIVATE 1
/FTId=VAR_000299.
K -> E (IN STHE).
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Y -> C (IN STHE).
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Pred. No. 3.9e-1
8; Mismatches
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InterPro; IPR0001188; GABAA, recepto
InterPro; IPR001175; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BINDING
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TIGREAMS; TIGRO0860; LIC; 1.
PROSITE; PS00236; NEUROTR ION_CHANNEL;
Receptor; Postsynaptic membrane; Ionic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SUBCELLAULAR LOCATION: Integral membrane protein.
MISCELLAURAE LOCATION: INTEGRAL MEMBRANE STRYCHNINE.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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GETTRKLYV
                                HHKSPMLNLFQEDEAGEGRFNFSAYGMGPACLQAKDGISVKGANNSNTTNP-PPAP-SKS
                                                    SSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRDEKDLGCCTKHY
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BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

OLIVED (GLCNAC...

STRYCHNINE (OR 230)

STRYCHNINE (OR 25)
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Pred. No. 4.4e
8; Mismatches
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GLYCINE RECEPTOR ALPHA-1 CHAIN
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    channel; Glycoprotein;

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(BY SIMILARITY).
(BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre European Bioinformatics Institute. There are no restitute the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning, expression and electrophysiological characterization of glycine receptor alpha subunit from zebrafish.";
Neuroscience 90:303-317(1999).
-I- FÜNCTION: THE GLYCINE RECEPTOR IS A NEUROTRANSMITTER-GATED ION CHANNEL. BINDING OF GLYCINE TO ITS RECEPTOR INCREASES THE CHLOICE CONDUCTANCE AND THUS PRODUCES HYPERPOLARIZATION (INHIBITION OF CONDUCTANCE AND THUS PRODUCES HYPERPOLARIZATION (INHIBITION OF
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                  EMBL; AJ005812; CAA06711.1; ZFIN; ZDB-GENE-991117-1; gl
                                                                                        DOMAIN
                                                                                                                                                DOMAIN
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Bregestovski P., Korn H.;
                                                                             TRANSMEM
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                                                                                                                                                                                       l'ransmembrane;
                                                                                                                                                                                                                                             PRINTS; PR00252; NRIONCHANNEL.
                                                                                                                                                                                                                                                                                     InterPro; IPR000188; GABAA_receptor.
InterPro; IPR001175; Neur_channel.
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15-JUN-2002
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MISCELLANEOUS; HIGHLY SENSITIVE TO ACTIVATION BY TAURINE DESP
THE PRESENCE OF A VALINE IN POSITION 135. IN MAMMALS VALINE A
THIS POSITION CAUSES A DRASTIC LOSS OF TAURINE EFFICACY.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: EXPRESSED IN BRAIN.
MISCELLANEOUS: THIS RECEPTOR IS ACTIVATED BY GLYCINE
ANTAGONIZED BY STRYCHNINE. CAN ALSO BE ACTIVATED BY G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEURONAL FIRING)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BRARE
                                                                                                                                                                                                                                                         PF02931; Neur_chan_LBD; 1.
PF02932; Neur_chan_memb; 1.
                                                                                                                                                                                                   PS00236; NEUROTR_ION_CHANNEL; Postsynaptic membrane; Ionic
                                                                                                                                                                                                                                  TIGR00860; LIC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 41, Last annotation updat
                                                                                                                                                                                       Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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    BY SIMILARITY.
N-LINKED (GLCNAC.
STRYCHNINE (OR 226
STRYCHNINE (OR 221)
                                                                                       POTENTIAL.
CYTOPLASMIC
                                                                                                                                                          POTENTIAL.
GLYCINE RECEPTOR,
                                                                           POTENTIAL
                                                                                                                    POTENTIAL.
                                                                                                                                POTENTIAL
                                                                                                                                             EXTRACELLULAR
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                                                             SIMILARITY.
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channel;
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                                                                                                                                              (POTENTIAL)
       226)
221)
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(BY SIMILARITY)
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RESULT 9
GRAL_MOUSE STANDARD; PRT; 457 AA.

AC 064018; Q64019; Q9ROY6; Q9ROY7;
D1 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
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DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
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DT 16-OCT-2001 (Rel. 40, Last sequence update)
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                                                                                                                                                                                                    Guenet J.L., Betz H.; "Structural analysis of mouse glycine receptor alpha subunit genes." "Structural analysis of mouse glycine receptor alpha subunit genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                      Ryan S.G., Buckwalter M.S., Lynch J.W., Handford C.,
Shiang R., Wasmuth J.J., Camper S.A., Schofield P.,
"A missense mutation in the gene encoding the alpha
inhibitory glycine receptor in the spasmodic mouse."
Nat. Genet. 7:131-135(1994).
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                                                               AND BETA (58
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InterPro; IPR000188; GABAA_recepto
InterPro; IPR001175; Neur_channel.
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or send an email to license@isb-sib.ch).
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SUBCELLULAR LOCATION: Integral membrane protein.

ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND ALTERNATIVE SPLICING.

SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.

SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.

SPASMODIC (SPD), A MOU MUTANT WHICH RESEMBLES TO THE HUMBER OF SPASMODIC (SPD), A MOU MUTANT WHICH RESEMBLES TO THE LOSEASE (STHE)).

HYPEREKPLEXIA (OR STARTLE DISEASE (STHE)).

MISCELLANEOUS: THE ALPHA SUBUNIT BINDS STRYCHNINE.

SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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MEDLINE-91367372; PubMed-1716350;
Akagi H., Hirai K., Hishinuma F.;
*Functional properties of strychnine-sensitive glycine receptors
*Functional properties of strychnine-sensitive glycine mRNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1988 (Rel. 07, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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GLRA1 OR GLYR.
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Grenningloh G., Kettenmann H., Be
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                                                                                                                                                                                                                                                                                       SEQUENCE OF 23-457 FROM N.A. (SHORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
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EMBL; Y00276; CAA68378.1; -.
EMBL; M63915; AAA63490.1; -.
EMBL; X55246; CAA38987.1; -.
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MEDLINE-91115810; PubMed-1703526;
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Biol. Chem. 266:2048-2053(1991).

- FUNCTION: THE GLYCINE RECEPTOR IS A NEUROTRANSMITTER-GATED ION CHANNEL. BINDING OF GLYCINE TO ITS RECEPTOR INCREASES THE CHLOIC CHANNEL. BINDING OF GLYCINE TO THE RECEPTOR INCREASES THE CHLOIC CHANNEL. BINDING OF GLYCINE TO THE RECEPTOR INCREASES THE CHLOIC CHANNEL. BINDING OF GLYCINE TO THE RECEPTOR INCREASES THE CHLOIC CHANNEL. BINDING OF GLYCINE TO THE RECEPTOR INCREASES THE CHLOIC CHANNEL. BINDING OF GLYCINE TO THE RECEPTOR INCREASES THE CHLOIC CHANNEL. BINDING OF GLYCINE TO THE RECEPTOR INCREASES THE CHLOIC CHANNEL. BINDING OF GLYCINE TO THE RECEPTOR INCREASES THE CHLOIC CHANNEL. BINDING OF GLYCINE TO THE RECEPTOR INCREASES THE CHLOIC CHANNEL. BINDING OF GLYCINE TO THE RECEPTOR INCREASES THE CHLOIC CHANNEL. BINDING OF GLYCINE TO THE CHANNEL. BINDING OF GLYCINE TO THE CHANNEL. BINDING OF GLYCINE TO THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANNEL THE CHANN
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SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
MISCELLANGOUS: THE ALPHA SUBUNIT BINDS STRYCHNINE.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL
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IPR001175; Neur_channel.
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1568.5; DB 1;
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01-FEB-1996 (Rel. 33, Last seque
15-JUN-2002 (Rel. 41, Last annotation of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the c
                                                                                                     Guenet J.-L., Kinse J., Betz H., Becker C.M.;
"The spastic mouse: aberrant splicing of glycine subunit mRNA caused by intronic insertion of L1 e Neuron 13:1003-1015(1994).

-!- FUNCTION: THE GLYCINE RECEPTOR IS A NEUROTRAN
                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND VARIANTS SPASTIC. STRAIN-C57BL/6, and BALB/c; TISSUE-Brain, MEDLINE-95033198; PubMed-7946325;
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NEURONAL FIRING).
SUBUNIT: PENTAMER COMPOSED OF SUBCELLULAR LOCATION: Integral
                                                             FUNCTION: THE GLYCINE RECEPTOR IS A NEUROTRANSMITTER-GATED CHANNEL. BINDING OF GLYCINE TO ITS RECEPTOR INCREASES THE CONDUCTANCE AND THUS PRODUCES HYPERPOLARIZATION (INHIBITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRLSYREYPDDSLDLDPSMLDSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KSPEEMRKLFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WKPDLFFANEKGAHFHEITTDNKLLRISRNGNVLYSIRITLTLACPMDLKNFPMDVQTCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPPVNVSCNIFINSFGSTAETTMDYRVNIFLRQQWNDPRLAYNEYPDDSLDLDPSMLDSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLSFLLLWTLPGQVLLRVALAKEEVKSGTKGSQPMSPSDFLDKLMGRTSGYDARIRPNFK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MQLE---
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                                                                                                                                                                                                        c.,
                                                                                                                                                                                                                                                                                                                                                                                                        S.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Mouse)
                                                                                                                                                                                                               Fischer M., Gass P.,
                                                                                                                                                                                                                                                                                                                                                                                                           Giros
                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=7920630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
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8
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Integral
                                                                                                                                                                                                                                                                                                                                                                                                           Suh D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleosto
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                             insertion.
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                      ALPHA AND
                                                                                                                                                                                                                                                                                                                                                                                                           Bieniarz M.,
                                                                                                                                                                                                             Simon-Chazottes
membrane
                                                                                                                                                                                                                                                                                                                                                                 mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
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(Glycine receptor 58
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                        BETA SUBUNITS
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                                                                                                                                                                                                                                                                                                                                                                 'n
                                                                                                                                                                                                                                                           Liver;
                                                                                                                                                                                                                                                                                                                                                                                                           Caron M.G.,
                                                                                                                                                   element.
                                                                                                                                                                                                                                                                                                                                                                 spastic mouse
                                                                                                                                                      receptor
element.";
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                                                                (INHIBITION
                                                                                 THE CHLORIDE
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TISSUE SPECIFICITY: HIGH LEVELS OF EXPRESSION IN CORTEX,

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В
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Best Local
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EMBL; X81202; CAA57076.1; -.
EMBL; X81201; CAA57075.1; -.
EMBL; X81204; CAA57075.1; -.
EMBL; L32594; AAA65966.1; -.
MGD; MGI:95751; G1rb.
InterPro; IPR000188; GABAA_receptor.
InterPro; IPR001175; Neur_channel.
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DISULFID
CARBOHYD
CARBOHYD
VARIANT
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CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF02931; Neur_chan_LBD; 1. Pfam; PF02932; Neur_chan_memb; 1. PRINTS; PR00252; NRIONCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIPPOCAMPUS, THALAMUS AND CEREBELLUM.
HIPPOCAMPUS, THALAMUS AND CEREBELLUM.
DISEASE: DEFECTS IN GLRB CAUSE THE SPASTIC CONDITION WHICH
CHARACTERIZED BY MUSCLE RIGIDITY, TREMORS, MYOCLONIC JERKS,
PRONOUNCED STARTLE REACTION, ABNORMAL GAIT AND IMPAIRED RIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                         178
                                                                                                                                                               167
                                                                                                                                                                                                        120
                                                                                                                                                                                                                                              801
                                                                              227
                                                                                                                                                                                                                                                                                    63
                                                                                                                                                                                                                                                                                                                                                                                                                                                        188;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                             -SYREYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRL 166
                                                                                                                                                                                                                                                                                                                             LMGRTSGYDARIRPNFKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRL---
                                                                                                                                                                                                                                                                                                                                                                                                            LSFLLLWTLPGQVLLRVALAKEEVKSGTKGSQ------PMSPSDFLDK
                                          L-EKIALPQFDIKKEDIEYGNCTKYYKGTGYYTCVEVIFTLRRQVGFYMMGVYAPTLLIV
                                                                                                                         SITLSCPLDLTLFPMDTQRCKMQLE----
                                                                                                                                                             TLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQ
                                                                                                                                                                                                      SDFR--GSDALTVDPTMYKCLWKPDLFFANEKSANFHDVTQENILLFIFRDGDVLVSMRL
                                                                                                                                                                                                                                                                                                                                                                   ISFFILMSL----LFEDACAKEKSSKKGKGKKKQYLCPSQQSPEDLARVPPNSTSNILNR
                                                                                                                                                                                                                                                                                    LL---VSYDPRIRPNFKGIPVDVVVNIFINSFGSIQETTMDYRVNIFLRQKWNDPRLKLP
ILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLFVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGR00860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     365
496 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disease mutation.

1 22 BY S
23 496 GLYC
23 265 EXTH
66 290 PROB
99 316 PROB
31 354 PROB
31 354 CYTC
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151
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197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 871; DB 1;
Pred. No. 1.3e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISSING (IN SPASTIC 2).
R -> A (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
NFKGIPVDV -> TTMLDIQPMI (IN SPASTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (PROBABLE). PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLYCINE RECEPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LFFANEKSA -> VSMSWIYNR (IN SPASTIC 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISSING (IN SPASTIC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   555FDFA8918437BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.
channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                    87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 496
                                                                                                                       SFGYTTDDLRFIWQSGDP-VQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPASTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IS
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                                                                                                  Query Match
Best Local
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01-FEB-1991
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRB_RAT P20781;
                                                                                                                                                 CARBOHYD
CARBOHYD
                                                                                                                                                                                                                         TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND PARTIAL S
MEDLINE=90297968; PubMed=2163264;
Grenningloh G., Pribilla I., Prio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Glycine receptor beta chain precursor (Glycine receptor 58 kDa
                                                                                                                                                                         TRANSMEM DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glycine receptor.";
Neuron 4:963-970(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            subunit).
                                                                                                                                                                                                                                                                                                                           TIGRFAMS;
                                                                                                                                                                                                                                                                                                                                                   pfam; PF02931; Neur_chan_LBD; 1.
pfam; PF02932; Neur_chan_memb; 1.
                                                                                                                                                                                                                                                                                                                                                                            PIR; JH0165; JH0165.
InterPro; IPR000188; GABA;
InterPro; IPR001175; Neur_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                                                                                                                                     SEQUENCE
                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                        Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Taleb O., Betz H.;
                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                    Receptor; Postsynaptic
                                                                                                                                                                                                                                                                                                                 PROSITE; PS00236; NEUROTR_ION_CHANNEL;
                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION:
-!- SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and expression of the 58 kd beta subunit of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEURONAL FIRING).
SUBUNIT: PENTAMER COMPOSED OF ALPHA (48 kDa) AND BETA (58 kDa)
SUBUNITS. A THIRD TYPE OF SUBUNIT (93 kDa) IS A PERIPHERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: THE GLYCINE RECEPTOR IS A NEUROTRANSMITTER-GATED ION CHANNEL. BINDING OF GLYCINE TO ITS RECEPTOR INCREASES THE CHLORIDE CONDUCTANCE AND THUS PRODUCES HYPERPOLARIZATION (INHIBITION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                             RECEPTOR CORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEMBRANE PROTEIN ASSOCIATED WITH THE CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   342 ASLVEYAVVQVMLNNPK---RVEAEKRR 366
                                                                                     187;
             51
                                                            9
                                                                                                                                                                                                                                                                                                                                          PR00252;
                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LMGRTSGYDARIRPNFKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRL---
                                    VSFFILMSL----LFEDACSKEKSSKKGKGKKKQYLCPSQQSAEDLARVPPNSTSNILNR
                                                          LSFLLLWTLPGQVLLRVALAKEEVKSGTKGSQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AALLEYAAINFVSRQHKEFIRLRRRQRR
                                                                                                                                                                                                                                                                                                                             TIGR00860; LIC;
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                                                                                     Conservative
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55927
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496
265
290
316
316
477
495
197
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                                                                                                38.3%;
47.8%;
                                                                                                                                                                                                                                                                                                                                                                                          GABAA_receptor.
                                                                                                                                                                                                                                                                                                     membrane; Ionic
                                                                                                                                                                                                                                                                                                                                                                                                                   N: Integral membrane TO THE LIGAND-GATED
                                                                                                                                     WW;
                                                                                                                                                                                                                                                                                                                                                                              channel.
                                                                                      63;
                                                                                                                                   PROBABLE.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (PO'

N-LINKED (GLCNAC. . .) (PO'

N-LINKED (GLCNAC. . .) (PO'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prior P., Multhaup G.,
                                                                                                  Pred.
                                                                                                            Score 863.5;
                                                                                                                                                                                                                                                 GLYCINE RECEPTOR BETA CHAIN. EXTRACELLULAR (PROBABLE).
                                                                                                                                                                                                 CYTOPLASMIC
                                                                                                                                                                                                               PROBABLE
                                                                                                                                                                                                                                       PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                   Mismatches
No. 5.7e-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           372
                                                                                                                                                (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                    channel; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
                                                                                                                                                                                                 (PROBABLE)
                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                    protein.
IONIC CHANNEL FAMILY
                                                                                   88;
                                                                                     Indels
                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beyreuther
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAINS OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the inhibitory
                                                                                                              496;
                                                            - PMSPSDFLDK
                                                                                     53;
                                                                                                                                                                                                                                                                                                     Signal
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                                                                                     Gaps
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              107
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RESULT 13
GRB_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRB_HUMAN P48167;
                                                                                                                                                                                                                                                                                                                          and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1996 (Rel. 33,
01-FEB-1996 (Rel. 33,
15-JUN-2002 (Rel. 41,
Glycine receptor beta
                                 use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                   the
                                                                                                                                                                                                              "The human glycine receptor beta subur refined chromosomal localization, and Genomics 50.341-345(1998).
                                                                                                                                                                                                                                              MEDLINE-98341117; PubMed-9676428;
Milani N., Muelhardt C., Weber R.G., Lichter P., Kioschis
Poustka A., Becker C.-M.;
                                                                                                                                                                                                                                                                                                             Brain
                                                                                                                                                                                                                                                                                                                                   Handford C.A., Lynch J.W., Baker E., Sutherland G.R., Schofield P.R.; "The human glycine receptor beta subtfunctional characterisation and chron
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Hippocampus;
MEDLINE-96352561; PubMed-8717357;
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                               SUBCELLULAR LOCATION: Integral membrane SIMILARITY: BELONGS TO THE LIGAND-GATED
                                                                                                                                                   FUNCTION: THE GLYCINE RECEPTOR IS A NEUROTRANSMITTER-GATED I CHANNEL. BINDING OF GLYCINE TO ITS RECEPTOR INCREASES THE CI CONDUCTANCE AND THUS PRODUCES HYPERPOLARIZATION (INHIBITION NEURONAL FIRING).

SUBUNIT: PENTAMER COMPOSED OF ALPHA AND BETA SUBUNITS.
                                                                                                                                                                                                                                                                                                                          murine
                                                                                  European
                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223
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                                                                                                                                                                                                                                                                                                            Res. Mol. Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AALLEYAAI - - - - NFVSRQHKEFIRLRRRQR 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L-EKIALPQFDIKKEDIEYGNCTKYYKGTGYYTCVEVIFTLRRQVGFYMMGVYAPTLLIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SITLSCPLDLTLFPMDTQRCKMQLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDFR--GSDALTVDPTMYKCLWKPDLFFANEKSANFHDVTQENILLFIFRDGDVLVSMRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -SYREYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LL---VSYDPRIRPNFKGIPVDVVVNIFINSFGSIQETTMDYRVNIFLRQKWNDPRLKLP
                                                                                                                                                                                                                                                                                                                                                                                                                                 s (Human).
Metazoa; Chordata; C
Metazoa; Primates; (
                                                                                                                                                                                                                                                                                                                          genes.";
                                                                          Swiss Institute or Bioinformatics Institute.
            AAB37750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence up
Last annotation
chain precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                             Res. 35:211-219(1996)
                                                                                                                                                                                                                                                                                                                                    beta subunit: p
and chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; | Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                          , and population
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                     Webb G.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Glycine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 497
                                                                               There are no restrictions
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                                                                                                                                                                                                                                                                                                                                              primary
                                                                     as its content
                                                                                                                               protein.
IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                     localisation
                                                         Usage
                                                                                                                                                                                                                          (GLRB): structure, lon polymorphism.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor
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                                                          bу
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Best Local S
Matches 186
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TIGREAMS; Trum.
TOSITE; PS00236; P
                                                                          01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Gamma-aminobutyric-acid receptor beta subun
                                                                                                                               GAB_LYMST P26714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM TRANSMEM
                   Lymnaea stagnalis (Great Eukaryota; Metazoa; Mollu Lymnaeidae; Lymnaea. MCBI_TaxID=6523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pfam; PF02931; Neur_chan_LBD;
pfam; PF02932; Neur_chan_memb;
PRINTS; PR00252; NRIONCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000188; GABAA_receptor
InterPro; IPR001175; Neur_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM; 138492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF094755; AAC71034.1; Genew; HGNC:4329; GLRB.
                                                                      receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane
EQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 38.0%;
Local Similarity 47.4%;
mes 186; Conservative
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                                                                                                                                                                                                                                                               VILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLFV
                                                                                                                                                                                                                                                                                                           KLMGRTSGYDARIRPNFKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM
                                                                                                                                                                                                                                                   VVLSWLSFWINPDASAARVPLGIFSVLSLASECTTLAAELPKVSYVKALDVWLIACLLFG
                                                                                                                                                                                                                                                                                                                                                                     LTLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAV
                                                                                                                                                                                                                                                                                                                                                                                              PSDFR--GSDALTVDPTMYKCLWKPDLFFANEKSANFHDVTQENILLFIFRDGDVLVSMR
                                                                                                                                                                                                                                                                                                                                                                                                                   --SYREYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIR 165
                                                                                                                                                                                                                                                                                                                                                                                                                                            RLL---VSYDPRIRPNFKGIPVDVVVNIFINSFGSIQETTMDYRVNIFLRQKWNDPRLKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLSFLLLWTLPGQVLLRVALAKEEVKSGTKGSQPM--------
                                                                                                                                                                                                     FASLVEYAVVQVMLNNPKRVEAEKARIAKAEQ
                                                                                                                                                                                                                           FAALLEYAAI ----NFVSRQHKEFIRLRRRQR
                                                                                                                                                                                                                                                                                                QL-EKIALPQFDIKKEDIEYGNCTKYYKGTGYYTCVEVIFTLRRQVGFYMMGVYAPTLLI
                                                                                                                                                                                                                                                                                                                                               LSITLSCPLDLTLFPMDTQRCKMQLE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Postsynaptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGR00860; LIC; 1.
PS00236; NEUROTR_ION_CHANNEL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 242
497
 N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                           STANDARD;
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497
265
290
316
354
478
478
496
197
197
242
56122
                                             Great pond Mollusca;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW;
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GLYCINE RECEPTOR BETA CHAIN.
THE PROPOSED OF THE PROPOSED OF THE PROPOSED OF THE PROPOSED OF THE PROPOSED OF THE PROPOSED OF THE PROPOSED OF THE PROPOSED OF THE PROPOSED OF THE PROPOSED OF THE PROPOSED OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 855.5; DB pred. No. 2.7e-65
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N-LINKED (GLCNAC. . .) (POTENTIAL)
C1F0B407601D3625 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROBABLE.
BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROBABLE.
                                             snail).
Gastropoda;
                                                                                                                                            PRT;
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                                                                                update)
subunit
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channel; Glycoprotein; Signal;
                                                                                                                                           A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PROBABLE)
                                                                                                                                                                                                    372
                                                                                                                                                                                                                           371
                                               Pulmonata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; 88
                                                                                  precursor
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-SFGYTTDDLRFIWQSGDP-V

221

225 176

283

280

343

Basommatophora;

(GABA(A)

Indels Length 497;

53;

SPSDFLD Gaps

49

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Best Local S
Matches 146
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PIR; S17785; S17785.
InterPro; IPR000188; GABAA_receptor.
InterPro; IPR001175; Neur_channel.
Pfam; PF02931; Neur_chan_memb; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
                                                                                                                                                                                                                                                                                                                  CARBOHYD
DISULFID
                                                                                                                                                                                                                                                                                                                                           CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
DOMAIN
TRANSMEM
CARBOHYD
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-92007774; PubMed-1655414;
Harvey R.J., Vreugdenhil E., Zaman S.H., Bhandal N.S.,
Usherwood P.N.R., Barnard E.A., Darlison M.G.;
"Sequence of a functional invertebrate GABAA receptor
can form a chimeric receptor with a vertebrate alpha s
                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Postsynaptic membrane; Ionic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHANNEL. SUBUNIT: GENERALLY PENTAMERIC.
                          277
                                                   198
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                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00236; NEUROTR_ION_CHANNEL;
                                                                                                                                                 YIPSLLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWM
                                                                                                                NGNVLYSIRLTLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVF
                                                                                                                                                                                                   IDSLL---KGYDIRLRPSFGGAPLEIGIEVILASFDSISEVDMDYTITMYLNQYWRDERL
                                                                                                                                                                                                                 LDKLMGRTSGYDARIRPNFKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRL
:| |: || | : : : | | | | | | | | | | |
YWLNDRGAVTGVEDVSLPQFSITNYATIN-KIEELSTGDYQRLSLIFQLQRNIGYFIFQT
                                                                EWLEDAPAVQVAEGLTLPQFILRDEKDLGCCTKHYNTGKFTCIEVKFHLERQMGYYLIQM
                                                                                                   NGSLVYGMRFTTTLACMMDLHNYPLDHQECTVEIE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR00860; LIC;
                                                                                                                                                                                                                                                                                                     24
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167
                                                                                                                                                                                                                                                      Conservative
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Pred. No. 1.
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N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAMMA-AMINOBUTYRIC-ACID RECEPTOR BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                      F81C9F2A850D62F4 CRC64;
                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                   SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THERE ARE FIVE TYPES GAMMA, DELTA, AND RHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein;
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                                                                                                                                                                                                                                                                DB 1;
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                                                                                                  -SYGYTMDDIVL
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                        336
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  316
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RESULT 15
GAB4_CHICK
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CARBOHYD
CARBOHYD
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-i- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO TO GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-91162222; PubMed-1848280;
Bateson A.N., Lasham A., Darlison M.G.;
"Gamma-aminobutyric acid A receptor heterogeneity
alternative splicing of a novel beta-subunit gene
J. Neurochem. 56:1437-1440(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X56647; CAA39969.1; -.
EMBL; X56648; CAA39970.1; ALT_SEQ.
PIR; JH0360; JH0360.
PIR; JH0359; JH0359.
InterPro; IPR000188; GABAA_receptor.
InterPro; IPR001175; Neur_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (Chicken)
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gamma-aminobutyric-acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001175; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P24045;
          CARBOHYD
                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                         Postsynaptic membrane; Ionic channel; Glycoprotein; Signal; Multigene family; Transmembrane; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00252; NRIONCHANNEL. TIGREAMS; TIGR00860; LIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9031;
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                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00236; NEUROTR_ION_CHANNEL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHANNEL.
SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO. SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; BETA-4 AND BETA-4' (SHOWN HARE PRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      337
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N-LINKED
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                                                                                                                                                                                                                                                            GAMMA-AMINOBUTYRIC-ACID RECEPTOR BETA-4
                                                                              PROBABLE.
                                                                                                      CYTOPLASMIC (PROBABLE)
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(POTENTIAL).
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1: sp_archea:*
2: sp_bacteria
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7: sp_mhc:*
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1 MTTLVPATLSFLL
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Gapop 10.0 ,
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Listing first 45 summaries
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sp_bacteria:*
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Q9gkf0 bos taurus
Q9gke9 bos taurus
Q8gy93 brachydanio
Q90w14 brachydanio
Q90w13 brachydanio
Q90wt3 brachydanio
Q9des8 brachydanio
Q9gy14 bos taurus
Q9gy14 sepia offic
Q46124 haemonchus
Q77295 drosophila
Q94900 drosophila
Q94900 drosophila
Q94900 drosophila
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                                                                                                                                             Q8vhf3 mus musculu
Q9des9 brachydanio
Q99jc9 rattus norv
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30.6	30.7	30.9	30.9	31.1	31.1	31.1	31.3	31.3	31.4	31.4	31.5	31.5	31.6	31.6	31.7	•	31.8		31.9	32.0	32.0	32.1	32.1		32.2	2	32.3	32.4
484	435	657	478	519	657	478	379	1106	351	336	416	416	494	550	541	430	454	421	454	601	430	430	456	533	496	481	606	606
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090990	Q9TYG6	017547	017548	Q9DDD9	Q9TW41	Q95PJ6	096964	Q22637	Q25634	Q9GQ52	Q17367	Q95Q96	Q9XZWO	017145	Q9U9B8	Q90590	Q961R4	046123	Q9VDU5	P92138	Q17369	Q95Q97	Q9GQ53	Q16896	018468	018471	Q9BLY8	Q9vsv0
Q9u990 caenorhabd	Q9tyg6 haemonchus	017547 caenorhabd	017548 caenorhabdi	Q9ddd9 brachydanio		Q95pj6 caenorhabd	O96964 ascaris	Q22637 caenorhabdi		Q9gq52 drosophila	Q17367 caenorhabd	Q95q96 caenorhabdi	Q9xzw0 heliothis	017145 lucilia	o	Q90590 gallus gal	Q961r4 drosophila	O46123 haemonchus		Ф.	Q17369 caenorhabd	~	3 drosc	Q16896 aedes a	O18468 heliothis	018471 heliothis		Q9vsv0 drosophila
abdi	hus	abdi	abdi	danio	abdi	abdi	suu	abdi	rca	ila	abdi	abdi	is v	cup	is c	gall	11a	hus	ila	ila	abdi	abdi	ila	aegyp	is v	is v	ila	ila

ALIGNMENTS

RESULT 1

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                                                                                                                             Q8VHF3
                                                              Query Match
Best Local S
Matches 358
                                                                                                                           Receptor.
SEQUENCE
                                                                                                                                                    Interpro; IPR000188; GABAA_receptor.
Interpro; IPR001175; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
TIGRFAMS; TIGR00860; LIC; 1.
PROSTIE; PS00236; NEUROTR_ION_CHANNEL; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-B6C3/FE; TISSUE=SPINAL CORD;
Groemer T.-W.W., Becker C.-M.M., Becker K.;
"Localization of different glycine receptor isoforms in murine spinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QBVHF3 PRELIMINARY; PRT; 416 AA.
QBVHF3;
Q1-MAR-2002 (TrEMBLrel. 20, Created)
Q1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
G1ycine receptor alpha 4 subunit.
                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                  Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases EMBL; {\sf AF462147}; {\sf AAL69899.1}; -
                                                                                                                                                                                                                                                                                                      cord. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLRA4
                                                              y Match 83.7%; Score 1886; DB 11; Local Similarity 91.8%; Pred. No. 3.7e-169; hes 358; Conservative 10; Mismatches 8;
416 AA;
                                                                                                                           48322 MW; C095998F4C077451 CRC64;
                                                                                            Length 416;
                                                                14;
                                                              Gaps
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352 368 308 232

292

187 188

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PRESULT
OCCUPANT
OCCU
                                                                                                                                                                 Query Match
Best Local S
Matches 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ol-MAR-2001 (TrEMBLrel. 16, Created)
Ol-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Ol-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Glycine receptor alphaz2 subunit.
GLRA4A OR GLRA2 OR GLYR ALPHA.
Brachydanio rerio (Zebrafish) (Zebra danio).
Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9DES9;
Q9DES9;
01-MAR-2001
                                                                                                                                                                                                                                                                                         TIGREAMS;
PROSITE; F
PROSITE; F
                                                                                                                                                                                                                                                                                                                                              Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ404970; CAC16687.1;
ZEIN; ZDB-GENE-010410-3; glra4a.
InterPro; IPR000345; CytC_heme_bind.
InterPro; IPR000188; GABAA_receptor.
InterPro; IPR001175; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_LBD; 1.
PRINTS; PR01620; GABAARGAMMA.
PRINTS; PR01620; GABAARGAMMA.
PRINTS; PR01620; GABAARGAMMA.
PRINTS; PR01620; GABAARGAMMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Imboden M., de Saint Jan D., Leulier F., Korn H., Goblet C., Bregestovski P., "Isolation and Characterization of a alpha 2-type zebrafish Receptor Subunit.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=7955;
                                                                                                                                                     Local 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            347
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                                          69
      83
                                                                                    31
                                                                                                                            9
                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00190; CYTOCHROME_C; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FVFAALLEYAAINFVSRQHKEFIRLRRRQRRQRLEEDIIQESRFYFRGYGLGHCLQARDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIVILSWYSFWINMDAAPARVGLGITTYLTMTTQSSGSRASLPKYSYYKAIDIWMAVCLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YSIRLTLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WNDPRLSYREYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVL
                                                                                      LCFLYLW---
                                                                                                                                                                                                                                                                                         PS00236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FVFAALLEYAAVNFVSRQHKEFMRLRRRQRRQRMEEDIIRESRFYFRGYGLGHCLQARDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WNDPRLAYREYPDDSLDLNPSMLESIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVL
                                                                                                                                                                                                                                                   456
                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                         NEUROTR_ION_CHANNEL;
                                                                                                                                                                                                                                                 52674 MW;
                                                                                                                                                             77.7%; Score 1749.5; 78.8%; Pred. No. 3.16 tive 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                 62713B7F29999FBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       456
                                                                                                                                                                                  9.5; DB 13; Length 3.1e-156;
                                                                               -QKPMSPSDFLDKLMGRTSGYDARIRPNFKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                431
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                                                                                                                                                                 Indels
                                                                                                                                                                 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycine
                                                                                                                                                                 Gaps
                                          128
                                                                                                                       8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                          Query Match
Best Local 9
                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Concentration dependence of single channel currents the recombinant alpha 1 glycine receptors.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-i - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY -1 SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNE EMBL; AJ310838; CAC35982.1; -.
Interpro. Terronom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q99JC9 PRELIMINARY;
Q99JC9;
Q1-JUN-2001 (TrEMBLrel. 17,
Q1-JUN-2001 (TrEMBLrel. 17,
Q1-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                              Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR01620; GABAARGAMMA.
PRINTS; PR00252; NRIONCHANNEL.
TIGRFAMS; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL;
                                                                                                                                                                                                                                                                                   Transmembrane.
SEQUENCE 480 AA;
                                                                                                                                                                                                                                                                                                                             Glycoprotein; Ionic channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN; Beato M., Groot-Kormelink P.J., Colquhoun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycine receptor alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000188; GABAA_receptor.
InterPro; IPR001175; Neur_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     413
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                                       84
                                                                               69
                                                                                                                         27
                                                                                                                                                               9
                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RFVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLFVFAALLEYAAINFVSRQHKEFIRLRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRLSYREYPDDSLDLDPSMLDSIW 128
                                                                                                                                          LSFLLLWTLPGQVLLRVALAKEEVKSGTKGSQPMSPSDFLDKLMGRTSGYDARIRPNFKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LYVD 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLIVFAALLEYAAVNFVSRQHKEFIRLRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRLTLILISCLMDLKNFPMDIQTCTM
KPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRLTLILSCLMDLKNFPMDIQTCTM
                                          PPVNVTCNIFINSFGSIAETTMDYRVNIFLRQKWNDPRLAYSEYPDDSLDLDPSMLDSIW
                                                                                                                       LSGFYFWE----AALLLSLVATKETNSARSRSAPMSPSDFLDKLMGRTSGYDARIRPNFKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KQRRQRIEEDLVRESRGFYFRGYGLGHCLQTKDGTAVEGSSVFAPPPPVQVLYDGEAVRK
                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                       55555 MW;
                                                                                                                                                                                                                            71.0%;
71.5%;
                                                                                                                                                                                                       34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                   Score 1598; DB 11;
Pred. No. 6.2e-142;
""matches 49;
                                                                                                                                                                                                                                                                                                                             Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                       322478D9A3052299 CRC64;
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                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BY SIMILARITY).
                                                                                                                                                                                                       42;
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밁 Ş Вþ Ş

Gaps

83

189

204

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Q91XP5
Q91XP5;
Q1-DEC-2001
Q1-DEC-2001
Q1-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Glycine receptor alpha 3 subunit.
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-SPINAL CORD;
Noegel S., Becker C., Becker K.;
"Different glycine receptor isoforms cerebellum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                             PRINTS; PRO1620; GABAARGAMMA.
TIGREAMS; TIGRO0860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                       Local Similarity
les 311; Conserv
                                                                                                                                                                                                                                                                                                                                                                PF02931; Neur_chan_LBD; 1. PF02932; Neur_chan_memb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KHYNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPARVGLGITT.308
                                                                                            FSSYTKTTMDYRVNVFLRQQWNDPRLSYREYPDDSLDLDPSMLDSIWKPDLFFANEKGAN 141
                                                                                                                                                                         LLRVALAKEEVKSGTKGSQPMSPSDFLDKLMGRTSGYDARIRPNFKGPPVNVTCNIFINS 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QPPAPLLREGETTRKLYVD 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KRKNKTEAFALEKFYRFSDTDDEVRESRFSFTAYGMGPCLQAKDGYVPKGPNHAVQV---
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SLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRDEKDLGCCTKHYNTGKFTCIEV
                                                                                                                                                          LLLSLVATKETNSARSRSAPMSPSDFLDKLMGRTSGYDARIRPNFKGPPVNVTCNIFINS
                                                                                                                                                                                                                                                                                    463 AA;
                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                      53605 MW;
                                                                                                                                                                                                                                      70.1%;
73.0%;
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                                                                                                                                                                                                                         33;
                                                                                                                                                                                                                     Score 1578; DB 11;
Pred. No. 4.5e-140;
33; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         isoforms are expressed in murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                    889D67DE9B223605 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murinae;
                                                                                                                                                                                                                       40;
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Best Local S
Matches 307
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Transmembrane.
SEQUENCE 449
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                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: INTEGNAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
EMBL; AF268356; AAG41140.1; JOINED.
EMBL; AF268359; AAG41140.1; JOINED.
EMBL; AF268360; AAG41140.1; JOINED.
EMBL; AF268361; AAG41140.1; JOINED.
EMBL; AF268361; AAG41140.1; JOINED.
EMBL; AF268361; AAG41140.1; JOINED.
EMBL; AF268363; AAG41140.1; JOINED.
EMBL; AF268363; AAG41140.1; JOINED.
EMBL; AF268364; AAG41140.1; JOINED.
EMBL; AF268365; AAG41140.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Glycine receptor alpha 1 subunit isoform b.
                                                                                                                                                       PRINTS; PROVIDED:
TIGREAMS; TIGRO0860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
PROSITE: PS00236; NEUROTR_ION_CHANNEL; 1.
PROSITE: PS00236; NEUROTR_ION_CHANNEL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor associated with bovine myoclonus."; Mol. Cell. Neurosci. 17:354-363(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pierce K.D., Handford C.A., Morris R., Vafa B
Healy P.J., Schofield P.R.;
"A nonsense mutation in the alphal subunit of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLRA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21109390;
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                                                                             al Similarity
307; Conser
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                               LLLWTLPGQVLLRVALAKEEVKSGTKGSQPMSPSDFLDKLMGRTSGYDARIRPNFKGPPV
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                LYLWE----TIVFFSLAASKEAEAARSASKPMSPSDFLDKLMGRTSGYDARIRPNFKGPPV
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                                                                           69.7%; llarity 72.6%; Conservative 37
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                                                                                                                                          51676 MW;
                                                                           Score 1570; E
Pred. No. 2.5e
Pred. Mismatches
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                                                                             2.5e-139;
ches 53;
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                                                                                                            DB
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                                                                                                                                          CRC64;
                                                                                                         Length 449;
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Query Match Best Local (Matches

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                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PRO-
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IO)
EMBL; AF268366; AAG41141.1; JOINED.
EMBL; AF268359; AAG41141.1; JOINED.
EMBL; AF268369; AAG41141.1; JOINED.
EMBL; AF268361; AAG41141.1; JOINED.
EMBL; AF268361; AAG41141.1; JOINED.
EMBL; AF268362; AAG41141.1; JOINED.
EMBL; AF268363; AAG41141.1; JOINED.
EMBL; AF268363; AAG41141.1; JOINED.
EMBL; AF268364; AAG41141.1; JOINED.
EMBL; AF268365; AAG41141.1; JOINED.
EMBL; AF268365; AAG41141.1; JOINED.
EMBL; AF268365; AAG41141.1; JOINED.
                                                   InterPro; IPR000188; GABAA_receptor.
InterPro; IPR001175; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR01620; GABAARGAMMA.
PRINTS; PR00252; NRIONCHANNEL.
TIGREAMS; TIGR00860; LIC; 1.
PROSTIE; PS00236; NEUROTE, TON_CHANNEL; 1.
                                     Glycoprotein; Ionic channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                       "A nonsense mutation in the alphal subunit of the inhibitory glycine receptor associated with bovine myoclonus."; wol. Cell. Neurosci. 17:354-363(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9GKE9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9GKE9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE-21109390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TIEMBLIEL 16, Created)
(TIEMBLIEL 16, Last sequence update)
(TIEMBLIEL 21, Last annotation update)
eptor alpha 1 subunit isoform a.
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  AA;
    52607
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  MW.
                                       Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
F31C41BFC8786908 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В.,
                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN (BY SIMILARITY)
IONIC CHANNELS FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         427
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Query Match
Best Local S
Matches 302
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Best Local S
Matches 307
                                                                                                                                                                                                                                                                                                                             Q8QG93 PRELIMINARY; PRT; 459 AA.
Q8QG93;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
61ycine receptor alpha21L subunit.
Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                        Submitted (FEB-2002) to the EMBL/GenBank/DDBJ EMBL; AF488379; AAM00910.1; -.
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Devignot V., Prado
                                                                                                                                                                                                                                           Brain."
                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7955;
                                                                                                                                                                                             Receptor
                                                                                                                                                                                                                                                    Devignot V., Prado de Carvalho L., Bregestovski P.,
P.A. Novel Glycine Receptor aZl Subunit Variant in th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               409
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                                                        302;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 LLLWTLPGQVLLRVALAKEEVKSGTKGSQPMSPSDFLDKLMGRTSGYDARIRPNFKGPPV
                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRLTLILSCLMDLKNFPMDIQTCTMQLE
QGSKSDGTHKKGPPVNVTCNIFINSFGSIAETTMDYRVNIFLRQQWNDPRLAYSEYPDDS
              ------KGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRLSYREYPDDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GETTRKLYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HHKSPMLNLFQEDEAGEGRFNFSAYGMGPACLQAKDGISVKGANNSNTTNP-PPAP-SKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPARVGLGITTVLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRDEKDLGCCTKHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LFFANEKGAHFHEITTDNKLXRISRNGNVLYSIRITLTLACPMDLKNFPMDVQTCIMQLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEEMRKLFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RQR------LEEDIIQESRFYFRGYGLG-HCLQARDGGPMEG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NTGKFTCIEARFHLERQMGYYLIQMYIPSLLIVILSWISFWINMDAAPARVGLGITTVLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------SFGYTMNDL1FEWQEQG-AVQVADGLTLPQF1LKEEKDLRYCTKHY
                                                                                                                                                                                 459
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                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           430
                                                                                                                                                                               52330 MW;
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                                                                                                                                  69.18;
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                                                                                                                     43;
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Pred. No. 2.5e-139;
                                                                                                                                  Pred.
                                                                                                                                                  Score 1555.5;
                                                                                                                                                                               FFC97E289FA3404A CRC64
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                                                                                                                     Mismatches
                                                                                                                                   NO.
                                                                                                                                   9e-138;
                                                                                                                                                  DB 13;
                                                                                                                                                                                                                           databases
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                                                                                                                     Indels
                                                                                                                                                Length
                                                                                                                                                                                                                                                                       Goblet C.;
                                                                                                                                                                                                                                                      Zebrafish
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                                                                                                                    37;
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                                                                                                                  Gaps
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                             116
121
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RESULT OPEN ACCORD DE COMMENT OF THE                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 301; Conserv
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Q90W14;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Glycine receptor alphaZ3 subunit precursor.
GLRA3 OR GLYRALPHA3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Imboden M., Devignot V., Goblet C.;

"Phylogenetic relationships and chromosomal location of five distinct glycine receptor subunit genes in the teleost danio rerio.";

Dev. Genes Evol. 211:415-422(2001).

EMBL; AJ308516; CAC38837.1;

ZFIN; ZDB-GENE-020402-1; glra3.

InterPro; IPR000188; GABAA_receptor.

InterPro; IPR000188; GABAA_receptor.

InterPro; IPR001175; Neur_channel.

Pfam; PF02931; Neur_chan_memb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO1620; GABAARGAMMA.
TIGREAMS; TIGRO0860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21541038; PubMed=11685575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
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                              81
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                                                                                                                              LDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRLTLILSCLMDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARQHKELLREQR--RRRHLKEDEAGDGRESFAAYGMGPACLQAKDGMAIKGNNNNAPTST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ILRDEKDLGCCTKHYNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSWVSFWINMD
                                                    FSSVTKTTMDYRVNVFLRQQWNDPRLSYREYPDDSLDLDPSMLDSIWKPDLFFANEKGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NPPEKTVEEMRKLFI 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APLLREGETTRKLYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KNFPMDVQTCIMQLE------SFGYTMNDLIFEW-DEKGAVQVADGLTLPQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRISKNGNVLYSIRITLVLACPMDL
                        FGSTAETTMDYRVNIFLRQKWNDPRLAYSEYPDDSLDLDPSMLDSTWKPDLFFANEKGAH
                                                                                                                                                                                                                                                                                                                                              28
450 A
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                              A
                                                                                                                                                                                                                                                                                                                                           27 F
450 G
51636 MW;
                                                                                                                                                                                                                                                                 68.3%;
72.9%;
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                                                                                                                                                                                                                                         33;
                                                                                                                                                                                                                                   Score 1537.5; DB 13;
Pred. No. 2.9e-136;
3; Mismatches 54; I
                                                                                                                                                                                                                                                                                                                                              GLYCINE RECEPTOR ALPHAZ3 SUBUNIT; FDD64C009EF60EA0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                       Length 450;
                                                                                                                                                                                                                                      25;
                                                                                                                                                                                                                                      Gaps
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AC 090W
AC 090W
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OS Brac
OC EDWA
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C CYpri
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Best Local
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Q90WT3;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Q1ycine receptor alpha24 subunit (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Phylogenetic relationships and chromosomal location of five distinct glycine receptor subunit genes in the teleost danio rerio.";
Dev. Genes Evol. 21:415-422(2001).
EMBL; AJ308517; CAC38838.1; -.
ZFIN; ZDB-GENE-020402-2; glra4b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brachydanio rerio (Zebrafish) (Zebra danio).
Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF02931; Neur_chan_LBD; 1. Pfam; PF02932; Neur_chan_memb; 1 TIGRFAMS; TIGR00860; LIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21541038; PubMed=11685575;
Imboden M., Devignot V., Goblet C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Actinopterygii; Neopterygii; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLRA4B OR GLYRALPHA4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000188; GABAA_receptor.
InterPro; IPR001175; Neur_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     365
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                                                                                                                                                                                                                                                                                                                     GPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRLSYREYPDDSLDLDPSMLDSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00236; NEUROTR_ION_CHANNEL; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KFHLERQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPARVGLGITTVLTMTTOSSGSRA
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                        TKHYNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPARVGLGIT
                                                                                                     GPPVNVTCNIFINSFGSITETTMDYRLNVFLRQQWNDPRLAYKEYPDDSLDLDPSMLDSI
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                                                                               VQLE----
                                                                                                                                                                                  WKPDLFFANEKGANFHEVTTDNKLLRIFQNGNVLYSIRLTLILSCPMDLKNFPMDTQTCT
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426
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
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48503 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                        61.3%;
67.7%;
                                                                                                                                                                                                                                                                                                                                                                                               31;
                                                                            -SFGYTMNDLIFQWLDEGP-VQVADDLMLPQFVLKEEKDLGYC
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1381; DB 13; Pred. No. 1.5e-121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9187E20B8793234B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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RESULT OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCURRENCE OCCU
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Best Local S
Matches 189
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-!- SIMILARITY: BELONGS TO THE LIGAND-GATED
EMBL AJ404971; CAC16688.1; -
ZFIN: ZDB-GENE-010410-2; glrb.
Interpro; IPR000188; GABAA_receptor.
Interpro; IPR0001175; Neur_chan_el.
pfam; PF02931; Neur_chan_LED; 1.
pfam; PF02932; Neur_chan_LeD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Regional Passish.";

System of Zebrafish.";

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIM-
-!- SUBCELLULAR TOCATION: TO THE LIGAND-GATED IONIC CHANNELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
61ycine receptor betaZ subunit precursor (Fragment).
6LRB OR GLYR BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9DES8;
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01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGRFAMS; TIGR00860; LIC; 1
PROSITE; PS00236; NEUROTR_ION_CHANNEL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR01620; GABAARGAMMA.
PRINTS; PR00252; NRIONCHANNEL.
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Regional Distribution of Glycine Receptor mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lycoprotein; Ionic channel; Postsynaptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10
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         188
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                                                                                                                  NEPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQFI
                                                                                                                                                                                                                                                                      DARIRPNEKGPPVNVTCNIFINSESSVTKTTMDYRVNVFLRQQWNDPRLSY-REYPDDSL
                                                                                                                                                                                                                                                                                                                                                                                                     TVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLFVFAALLEYAAINFVSRQHKEFIRLR
                                                                                                                                                                                                                                              DSRIRPNFKGIPVEDKVNIFINSFGSIQETTMDYRVNIFLRQRWNDPRLRLPTDFKSDAL
                                                                                                                                                                                                                                                                                                                                                                LKGLILLMLLVQFSAEEGGKPKKGKKGKQVICPSQLSAEDLDRVPANSTSNILNRLLMTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        498 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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. 16, Last sequ.
. 21, Last anno
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n; Craniata; Verte
; Teleostei; Ostar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 876.5;
Pred. No. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
; 12436FC3344F0BBB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
         -SFGYTTKDLVFMWQSGDP-VQMDE-IALPQFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Matches
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C -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.

R EMBL; AF268376; AAG14347.1; -.

R EMBL; AF268367; AAG14345.1; JOINED.

R EMBL; AF268368; AAG14345.1; JOINED.

R EMBL; AF268369; AAG14345.1; JOINED.

R EMBL; AF268370; AAG14345.1; JOINED.

R EMBL; AF268371; AAG14345.1; JOINED.

R EMBL; AF268371; AAG14345.1; JOINED.

R EMBL; AF268373; AAG14345.1; JOINED.

R EMBL; AF268375; AAG14345.1; JOINED.

R EMBL; AF268375; AAG14345.1; JOINED.

R EMBL; AF268376; AAG14345.1; JOINED.

R EMBL; AF268378; AAG14345.1; JOINED.

R EMBL; AF268371; AAG14345.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O9GJS9 PKELLINIA....
O1-MAR-2001 (TrEMBLrel. 16, Cr
01-MAR-2001 (TrEMBLrel. 21, Lr
01-JUN-2002 (TrEMBLrel. 21, L
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein; Ionic Transmembrane. SEQUENCE 497 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR01620; GABAARGAMMA.
PRINTS; PR00252; NRIONCHANNEL.
TIGRRAMS; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001175; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibitory Glycine Receptor.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (MAY-2000) to THE TRANSPORT PROTEIN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Pierce K.D., Handford C.A.,
Healy P.J., Schofield P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLRB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Bovine Myoclonus is Caused by a
Inhibitory Glycine Receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus
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                                                             108
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                                                                                                                                                                                                                                                                                            9 LSFLLLWTLPGQVLLRVALAKEEVKSGTKGSQPM------SPSDFLDK
                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                    LMGRTSGYDARIRPNFKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRL---
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                           -SYREYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRL 166
                                                                                                                                                                                                                                        VAFFILISL----CIEEAYSKEKSSKKGKGKKKQYLCPSQQSAEDLARVPANSTSNILNR
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                                                                                                                  LL---VSYDPRIRPNFKGIPVDVVVNIFINSFGSIQETTMDYRVNIFLRQKWNDPRLKLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Bovine).
                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56039 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          channel;
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                                                                                                                                                                                                                                                                                                                                                                                         37.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   subunit.
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                       Pred. No. 1.865; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               Score 850.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Postsynaptic membrane; Receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82F140C115A887E6 CRC64;
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Subunit

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SIMILARITY).

497; 53;

Gaps

62

177

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RESULT 12
Q9GYU4
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Best Local :
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InterPro; IPR000188; GABAA_receptor.
InterPro; IPR001175; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PFNITS; PR01620; GABAARGAMMA.
PRINTS; PR01620; GABAARGAMMA.
PRINTS; PR01620; GABAARGAMMA.
PRINTS; PR01620; NEUROTR, ION_CHANNEL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Kirby R.R., Williamson R., Farley S.;
"GABA-A receptor gene sequence from the central cuttlefish, Sepia officinalis.";
cuttlefish, Sepia officinalis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9GYU4;
Q9GYU4;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein; Ionic channel; Postsynaptic membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sepia officinalis (Common cuttlefish).
Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea;
Sepildae; Sepia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GABA-A receptor beta subunit.
                                                                                                                                                                                                                                                                                                                                                       Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAEGLTLPQF-ILRDEKDLGCCTKHY-NTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIV
                                                                     IWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRLTLILICCLMDLKNFPMDIQTC
                                                                                                                                                         KGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRLSYREYPDDSLDLDPSMLDS
                                                                                                                                                                                        LKYIAMLVLKESTVLIVTLV---LLVGSYGDQSRFQNTTDTIERLL---KGYDIRLRPQF
                                                                                                                                                                                                          FROM
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                  TMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRDEKDLGC
                                                                                                                        EVQALRIGMEIIIASFDSISEVNMDYTITMYLNQYWTDERLVYSNDSDDNLTLTGDFAEK
                                                    IWVPDTFFANDKNSFLHDITEKNKMIRLFGNGSIVYGMRFTTTLACMMDLHYYPLDEQNC
                                                                                                                                                                                                                                                                                                                                   486 AA;
                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                     56640 MW;
                                                                                                                                                                                                                                                                                33.2%;
                                                                                                                                                                                                                                                               69;
                                                                                                                                                                                                                                                                                Score 747.5;
Pred. No. 8.8
                                                                                                                                                                                                                                                                                                                                     1FD6DBCEC1EC7257 CRC64;
                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein;
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 303
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Query Match
Best Local Similarity
Matches 148; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOL. Biochem. Parasitol. 103:129-140(1999).
-:- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE
-:- SIMILARITY: BELONGS TO THE LIGAND-GATED
EMBL; Y14234; CAA74623.1; --
INTEGRAC: IRRO00188; GABAA_receptor.
INTEGRO: IRRO01175; Neur_channel.
pfam; PF02931; Neur_chan_LBD; 1.
pfam; PF02931; Neur_chan_memb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haemonchus contortus (Barber pole worm).
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Trichostrongyloidea; Haemonchidae; Haemonchinae; Haemonchus.
NCBI_TaxID=6289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1998 (TrEMBLrel. 01-JUN-1998 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00252; NRIONCHANNEL.
TIGRFAMS; TIGR00860; LIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20017520; PubMed=10551358;
Jagannathan S., Laughton D.L., Critten C.L.,
Horoszok L., Wolstenholme A.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00236; NEUROTR_ION_CHANNEL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                          DLGCCTKHYNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPARV
                                                                                                                                           DSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRLTLILSCLMDLKNFPMDIQ
                                                                                                                                                                                                                                                                                          VNIYLRSISKIDDVNMEYSAHFTFREEWVDARLAYGRFEDESTEVPPFVVLATSENADQS
                                                                                                                                                                                                                                                                                                                               CNIFINSTSSVTKTTMDYRVNVFLRQQWNDPRLSYREYPDDSLDLDPSML------
                                                                                                                                                                                                                                                                                                                                                                          MLALICTVSTIMSAVEAKRKLKEQEIIQRIL---NNYDWRVRPRGLNASWPDTGGPVLVT
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GLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLFVFAALLEYAAINFVSRQHKE
                                       -TKYCTSKTNTGEYSCARVKLLLRREYSYYLIQLYIPCIMLLVVSWVSFWLDKDAVPARV
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Last annotation updat
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IONIC CHANNELS FAMILY.
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Best Local S
Matches 157
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InterPro; IPRO00188; GABAA_receptor.
InterPro; IPRO00175; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
TIGRFAMs; TIGR00860; LIC; 1.
TIGRFAMs; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Glycoprotein; Ionic channel; Postsynaptic membrane; Transmembrane.
SEQUENCE 453 AA; 51905 MW; COAD53FA6968CD2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidaa; Drosophilidae; Drosophila.
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Best Local Sim
Matches 154;
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STRAIN-OREGON R; TISSUE-HEAD;

MEDLINE-9635534; PubMed-8702744;

Cully D.F., Paress P.S., Liu K.K., Schaeffer J.I

"Identification of a Drosophila melanogaster gluentification of a 
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01-FEB-1997
01-FEB-1997
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-FEB-1997 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Glutamate-gated chloride channel.
GLUCL-ALPHA OR DROSGLUCL OR CG7535.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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TIGRRO860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Glycoprotein; Ionic Channel; Postsynaptic membrane; Transmembrane.
SEQUENCE 456 AA; 52347 MW; 4008E57657566B1C CRC64;
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FlyBase; FBgn0024963; GluC1-alpha,
InterPro; IPR000188; GBBAL_receptor.
InterPro; IPR001175; Neur_channel.
pfam; PF02931; Neur_chan_LBD; 1.
pfam; PF02932; Neur_chan_memb; 1.
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Local Similarity 42.3%;
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                          17:16:58
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Pred. No. 3.2e-60;
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Indels Length

Gaps

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E. S.	Query Match Query Match 39.6%; Score 650.2; DB 9; Length 1857; Best Local Similarity 70.1%; Pred. No. 1.1e-169; Best Local Similarity 70.1%; Pred. No. 1.1e-169; Matches 943; Conservative 0; Mismatches 348; Indels 54; Gaps 3; Matches 943; Conservative 0; Mismatches 348; Indels 54; Gaps 3; Oy 63 CCTCCTCAGGGTGGCCTTGGCAAAAAAGAAGAAACTTAGGAAAACAAAC	ory glycine receptions of the reception		the heckpressi	HSGLYRA1 linear ON -f. sapleng alpha-2 strychnine binding subunit of in receptor mRNA. N X52008 X52008.1 GI:31848 X52008.1 GI:31848 X52008.1 GI:31848 X52008.2 Gi:31848 X52008.3 Gi:31848 X52008.1 GI:31848 X52008.1 GI:31848 X52008.1 GI:31848 X52008.2 Gi:31848 X52008.1 GI:31848 X5200	PAAGGGAAGGAAACCACGGGAAACTCTACGTGGACTGAGCCAAGA
	Qy 1083 AGAATTCAATAGACTTTCAAGAGGCCCAAGAGGCCCAAGAGGCCCAAAGAGGCCCAAGAGGCCCAAGAGGCCCAAGAGGCCCAAGAGGCCCAAGAGGCCCAAGAGAGAGAGAGAGAGAAGA	843 AUCCATICATION CONTROL CONT	723 1065 783 1125	Qy 603 ATCTCTGTCACTTTCAGTTGGCTACACCATGAAAGACCTCGTGTTTTGAGTGGCTGGAAGA 662		

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1334 GCTTCAACTTCTGGCCTACGGCCATGGCCTGCCAGCCAAGAATGGAGTC 1207	D	89 AGGAAGTCAAATCTGGAACCAAGGGGTCCCAGCCCATGTCCCCCTCTGATTTCCTAGACA 148	В . У
AGAGGGCCCAGAGGCTTGGAGGAAGATATCATCCAGGAAGTC 	Db	Query Match 39.4%; Score 646.8; DB 4; Length 1744; Best Local Similarity 71.2%; Pred. No. 9.6e-169; Matches 956; Conservative 0; Mismatches 317; Indels 69; Gaps 5;	. Be
	Db	ANNSNITAPPAASKSPEMKKLPIQKAKKIDKISRIGFPMAFLIFNMFYWIIYKIVR REDVHNO" BASE COUNT 396 a 508 c 451 g 389 t ORIGIN	BASE
989 AGGCAATCGACATCTGGATGGCTGTGTGTGTGTGTTTGTGTTTCGCTGCCTTGCTGGAGT 1048	Qy Db	TLTLACEMDLKARPMDVQTCINQLESFGYTMADLIFERQEQGAVQVADGLTLPQFIIK EEKDLRYCTKHYNTKKETCIEARFHLERQMGYYLIQMYIPSLLIVILSMISFHINMDA APARVGLGITTVLTMTTQSSGSRASLERVSYVKAIDIRMAVCLLEVESALLEXAAVNF VSRQHKELLERERKRRHHKSPMLNLFQEDEAGEGRENESAYGMGPACLQAKDGISVKG	
929 TCACCATGACCACCCAGAGCTCTGGCTCCCGGGCCTCTTTGCCTAAGGTGTCCTACGTGA 988 	Qy	/db_xref="GI:10180959" /translation="MYSENTLRLYLWETIVFESLAASKEAEAARSASKPMSPSDFLDK /translation="MYSENTSULLFINSFGSIAETIMDYRVNIFIRQQWNDPRLA LMGRTSGYDARLIRPNFKOPPVNYSCNLFINSFGSIAETIMDYRVNIFIRQQWNDPRLA YNEYPDDSLDLDPSMLDSIWKPDLFFANEKGAHFHEITTDNKLLRISRNGNVLYSIRI	
869 CCTTCTGGATCAACATGGATGCTGCCCCTGCCCGTGTGGGCCTGGGCATCACCACCGTGC 928 	Qy . Db	<pre>/note="Glralins; alternatively spliced" /codon_start1 /product="glycine receptor alpha 1 subunit" /protein_id="AAG14346.1"</pre>	
809 GCTACTATCTGATTCAGATGTACATCCCCAGCCTACTCATCGTCATCCTGTCCTGGGTCT 868	Оу		
749 ACTACAACACAGGGAAATTCACCTGCATCGAGGTAAAGTTTCACCTGGAACGGCAGATGG 808	Db Qy	ce 11744 ce 11744 /organism="Bos taurus" /db_xref="taxon:9913"	FEAT
689 GGCTGACTCTGCCCCAGTTTATCTTGCCGGATGAGAAGGATCTAGGCTGTTGTACCAAGC 748	. Qy	Healy, P.J. and Schoffeld, P.R. Direct Submission L Submitted (17-MAY-2000) Neurobiology Pr Medical Research, 384 Victoria Street,	JO
629 CCATGAAAGACCTCGTGTTTGAGTGGCTGGAAGATGCTCCTGCTGCCAAGTGGCTGAGG 688 	Оу	MEDLINE 21109390 PUBMED 11178872 REFERENCE 2 (bases 1 to 1744) AUTHORS Pierce, K.D., Handford, C.A., Morris, R., Vafa, B., Dennis, J.A.,	REFE AU
569 TIGAGAGCTCATCCATACICIGCAGCCCTCTGCCAICTCTGTCACTTTCAGTTGGCTACA 628	Qy Db	Healy, P.J. and Schofield, P.R. A nonsense mutation in the alphal subunit of the receptor associated with bovine myoclonus Mol. Cell. Neurosci. 17 (2), 354-363 (2001)	TI.
509 TGTCCTGCCTGATGGACCTCAAGAACTTCCCCATGGACATCCAGACGTGCACGATGCAGC 568	ФФ	cia; Per 3., Deni	REFE
449 AGTTACTGCGCATCTTCAAGAATGGGAATGTGCTGTACAGCATCAGGCTGACCCTCATTT 508 	ОУ	DS . Bos taurus. NISM Bos taurus Eukaryota; Metazoa; Chordata; Craniat	KEYWOR SOURCE ORGA
389 CAGACCTCTTTGCTAATGAGAAAGGGGCCAACTTCCATGAGGTGACCACGGACAACA 448 	Qy Db	ON Bos taurus glycine receptor alpha 1 subunit (Glra1) cds, alternatively spliced. N AF268375.1 GI:10180958	ACCE: VERS:
329 GAGAATATĆCTGATGACTCTCTGGACCTCGATCCCTCCATGCTGGACTCTATCTGGAAGC 388 	Qy	T 14 375 AF268375	RESUL AF268 LOCUS
269 TGGACTACCGGGTGAATGTCTTCTTGCGGCAACAGTGGAATGACCCACGCCTGTCCTACC 328	Оу	1383 GCTATGGTCAGAAGATATCCACCAG 1407 	Оу
209 CCGTGAACGTGACCTGCAACATCTTCATCAACAGTTTCAGCTCCGTCACCAAGACCACAA 268 	Qу	1323 GGCTGTCTTCCCTTTCACTTTCCTCATCTTCAATATCTTCTACTGGGTTGTCTATAAAGT 1382 	Db Qy
149 AACTTATGGGGCGAACATCTGGATATGATGCCAGGATTCGGCCCAATTTTAAAGGCCCAC 208 	Qy	1263 AGGAGAAACCACGCGGAAACTCTACGTGGACTGAGCCAAGAGAATTGACACCATCTCCCG 1322	Qy Db

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GATGACTTGACTCTCCCTCAGTTTGTACTAAAGGAGAAAAGGATCTCGGCTACTGCACT
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OFVLKEEKDLGYCTKHYMTGKFTCIEVKPHLERQMGYYLLQMYJPSLLTVILSWYSFW
INMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIMMAVCLLIFPAALLEY
AAVNFYSRQHKEFIRLKKKQRRQRIEEDLVRESRGFYFRGYGLGHCLQTKGGTAVGGS
SVFAPPPPVQVLYDGEAVRKRFVDRAKRIDTISRAVFPLSFLIFNVFYWITYKVLRHE
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DFLDKLMGRTSGYDARIRPNFKGPPVNVTCNIFINSFGSITETTMDYRLNVFLRQQWN
DPRLAYSEYPDASLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFQNGNVL
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                                                                                                                                  EMBO J. 9
90183975
                                                                                                                                                                 Greiningloh,G., Schmieden,V., Schofield,P.R., Seeburg,P.H., Siddique,T., Mohandas,T.K., Becker,C.M. and Betz,H. Alpha subunit variants of the human glycine receptor: primary structures, functional expression and chromosomal localization
                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; V. Mammalia; Eutheria; Primates; Catarrhini; 1 (bases 1 to 1857)
                                                                                                                                                                                                                                                                            receptor mRNA.
X52008
X52008.1 GI:31848
                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                   glycine receptor;
                                                                                                                                             the corresponding genes
EMBO J. 9 (3), 771-776 (1990)
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388. .1746
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                                                                                                           Location/Qualifiers
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HIZ PAGE BLANK (USPTO)

BASE

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US-10-075-846-4 (1-431) x HSGLYRA1 (1-1857)
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                                                       ProAlaValGlnValAlaGluGlyLeuThrLeuProGlnPheIleLeuArgAspGluLys
                                                                                                                                                           ArgProAsnPheLysGlyProProValAsnValThrCysAsnIlePheIleAsnSerPhe
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AspLeuGlyCysCysThrLysHisTyrAsnThrGlyLysPheThrCysIleGluValLys
                                           CCA---GTGCAAGTTGCTGAAGGATTGACCCTGCCCCAGTTTATTTTGAAAGAAGAGAAG
                                                                                                                  LeuSerLeuSerValGlyTyrThrMetLysAspLeuValPheGluTrpLeuGluAspAla
                                                                                                                                                                                                                                       SerIleArgLeuThrLeuIleLeuSerCysLeuMetAspLeuLysAsnPheProMetAsp
                                                                                                                                                                                                                                                                                   CACGATGTCACCACTGACAACAAATTGCTACGGATTTCGAAAAATGGCAAAGTGCTCTAC
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YAAVNFYSRQHKEFLRIRROKRQNKEEDVTRESRFNFSGYGMGHCLQVKDGTAVKAT
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1 (bases 1 to 1359)
Beato, M., Groot-Kormelink, P.J., Colquhoun, D. Concentration dependence of single channel concentration dependence of receptors
                                                                                                                                                                                                                                                                                                                                                       glycine receptor alpha 2 precursor. Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Crani
Mammalia; Eutheria; Rodentia; Sciur
                                                                                                                                                                           Submitted (30-MAR-2001) Groot-Kormelink P. Pharmacology, The School of Pharmacy, 29/3 London, WClN lax, UNITED KINGDOM
                                                                                                                                                                                                                                                                                                                                                                                                                                RNO310837
Rattus norvegicus mRNA 1
AJ310837
AJ310837.1 GI:13548660
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                                                                                                                                                1. .1359
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                                                                                                                                                             Location/Qualifiers
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1368 342 1308

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precursor ROD 03-APR-2001

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Rappold-Hoerbrand
               (RAPP/)
                               26-MAR-1999;
                                              23-MAR-2000;
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                                              2000WO-EP02600
                                                                                                                                                                                (first entry)
                                                                                                                                                                encoding a human ataxia
                              99EP-0106343,
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Best Local :
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                                                                                                                                                                                                                                                                                                                                         present sequence encodes a human ataxia protein. The ataxia protein and polynucleotides are useful for diagnosing and treating disorders related to ataxia. Ataxia gene sequences are useful in gene therapy, and as diagnostic tools or reagents for identifying a characterizing genetic defect involved in the disorders and disease related to ataxia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-656166/63.
P-PSDB; AAB19336.
                                                                                                                                                                                                                                                                                                                         Sequence
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                                      AGTTTCAGCTCCGTCACCAAGACCACAATGGACTACCGGGGTGAATGTCTTCTTGCGGCAA
                                                                                                                                     CCCATGTCCCCCTCTGATTTCCTAGACAAACTTATGGGGCGAACATCTGGATATGATGCC
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  CAGTGGAATGACCCACGCCTGTCCTACCGAGAATATCCTGATGACTCTCTGGACCTCGAT
                                                                                      AGGATTCGGCCCAATTTTAAAGGCCCACCCGTGAACGTGACCTGCAACATCTTCATCAAC
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                          AGTTTCAGCTCCATCACCAAGACCACAATGGACTACCGGGTGAATGTCTTCTTGCGGCAA
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Pred. No. 0;
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Matches 511;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prepn. of N-terminal extracellular site protein - by culturi E.coli transformed by a plasmid comprising the tac promoter.
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CTCTGCCATCTCTGTCACTTTCAGTTGGCTACACCATGAAAGACCTCGTGTTTTGAGTGGC
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 Novel nucleic acid sequence encoding human ataxia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linked to the tac promoter, a ribosome binding sequence, the E. coli outer membrane protein OmpF signal peptide coding sequence and a sequence coding for the N-terminal extracellular site of either the gamma-aminobutyric acid (GABA) A receptor alpha-subunit or the glycine receptor alpha-subunit. This expression plasmid can be used to transform E. coll to produce an N-terminal extracellular site protein of ion channel direct binding type receptor.
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         GluValLysPheHisLeuGluArgGln
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GAAGAGAAGGATCTGAGATACTGCACCAAGCACTACAACACAGGTAAATTCACCTGCATT
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